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(12) United States Patent
Rikihisa**(10) Patent No.: US 10,393,741 B2****(45) Date of Patent: Aug. 27, 2019****(54) COMPOSITIONS AND METHODS FOR THE
DETECTION OF *ANAPLASMA PLATYS*****(71) Applicant: Ohio State Innovation Foundation,**
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Columbus, OH (US)**(*) Notice:** Subject to any disclaimer, the term of this
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See application file for complete search history.**(56) References Cited****U.S. PATENT DOCUMENTS**4,478,914 A 10/1984 Giese
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Primary Examiner — Gary B Nickol**Assistant Examiner** — Lakia J Jackson-Tongue**(74) Attorney, Agent, or Firm** — Meunier Carlin &
Curfman LLC**(57) ABSTRACT**Described herein are improved diagnostic tools for veteri-
nary and human use which can be used for serodiagnosing
A. platys in mammals, particularly in members of the
Canidae family and in humans. The diagnostic tools are a
group of outer membrane proteins of *A. platys* and variants
thereof, referred to hereinafter as the "OMP proteins", a
group of outer membrane proteins of *A. platys* and variants
thereof referred to hereinafter as the "P44 proteins", and
antibodies to the OMP proteins and the P44 proteins.**3 Claims, 39 Drawing Sheets****Specification includes a Sequence Listing.**

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- Non-final Office Action received in U.S. Appl. No. 15/174,643 dated Mar. 29, 2017, 45 pages.
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* cited by examiner

Figure 1A

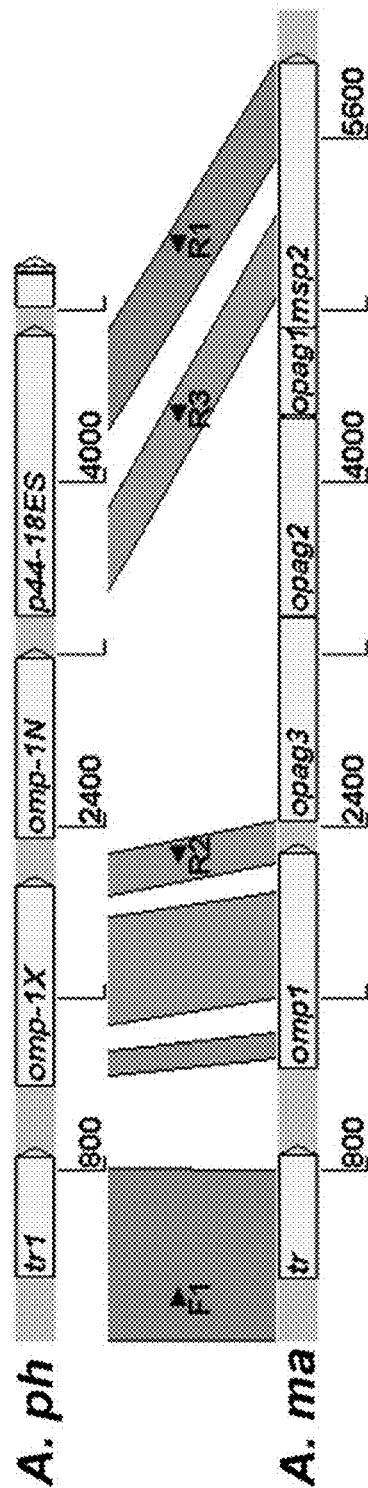
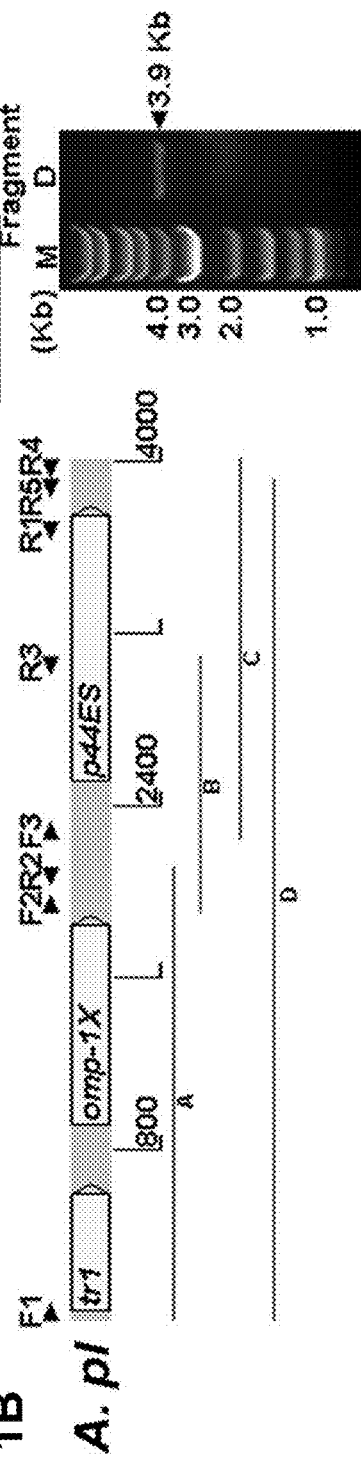


Figure 1C



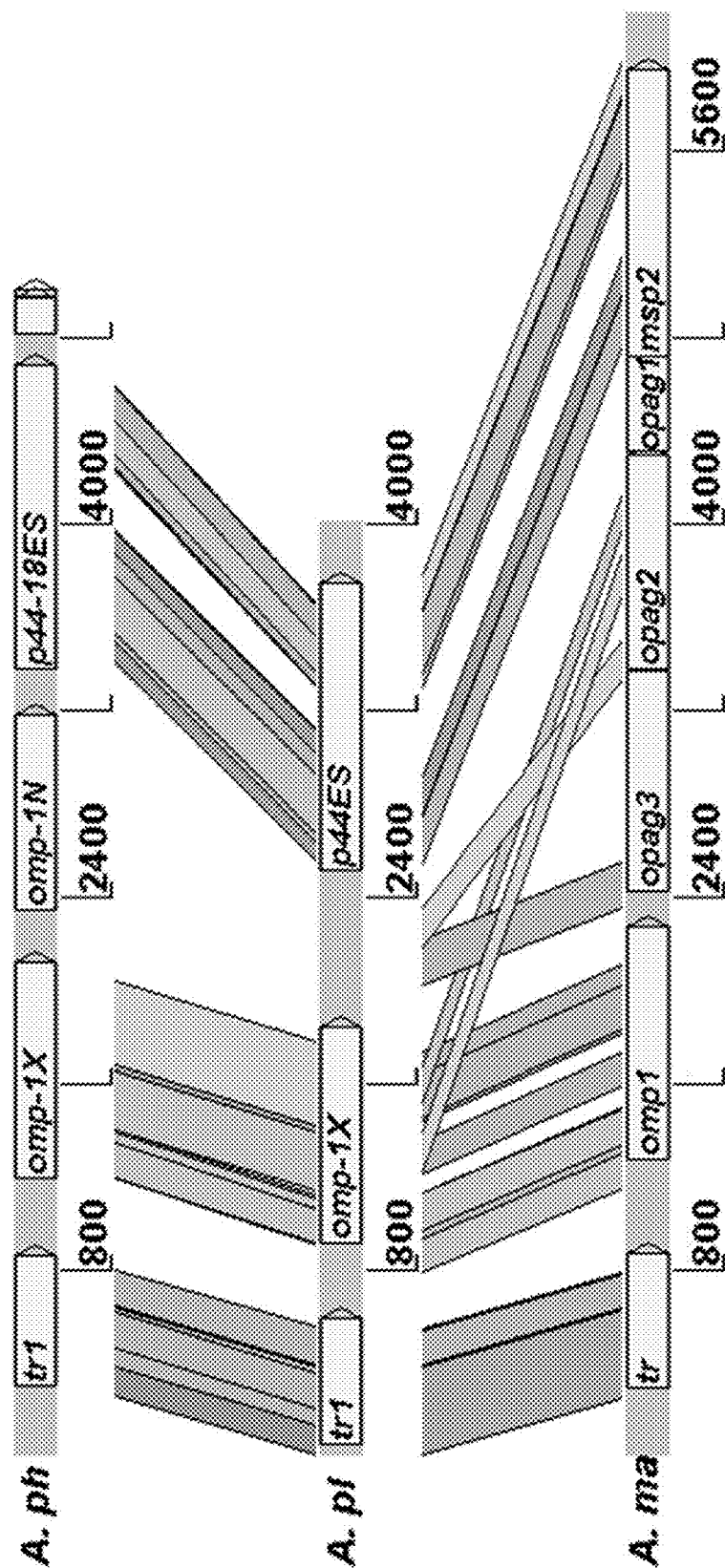


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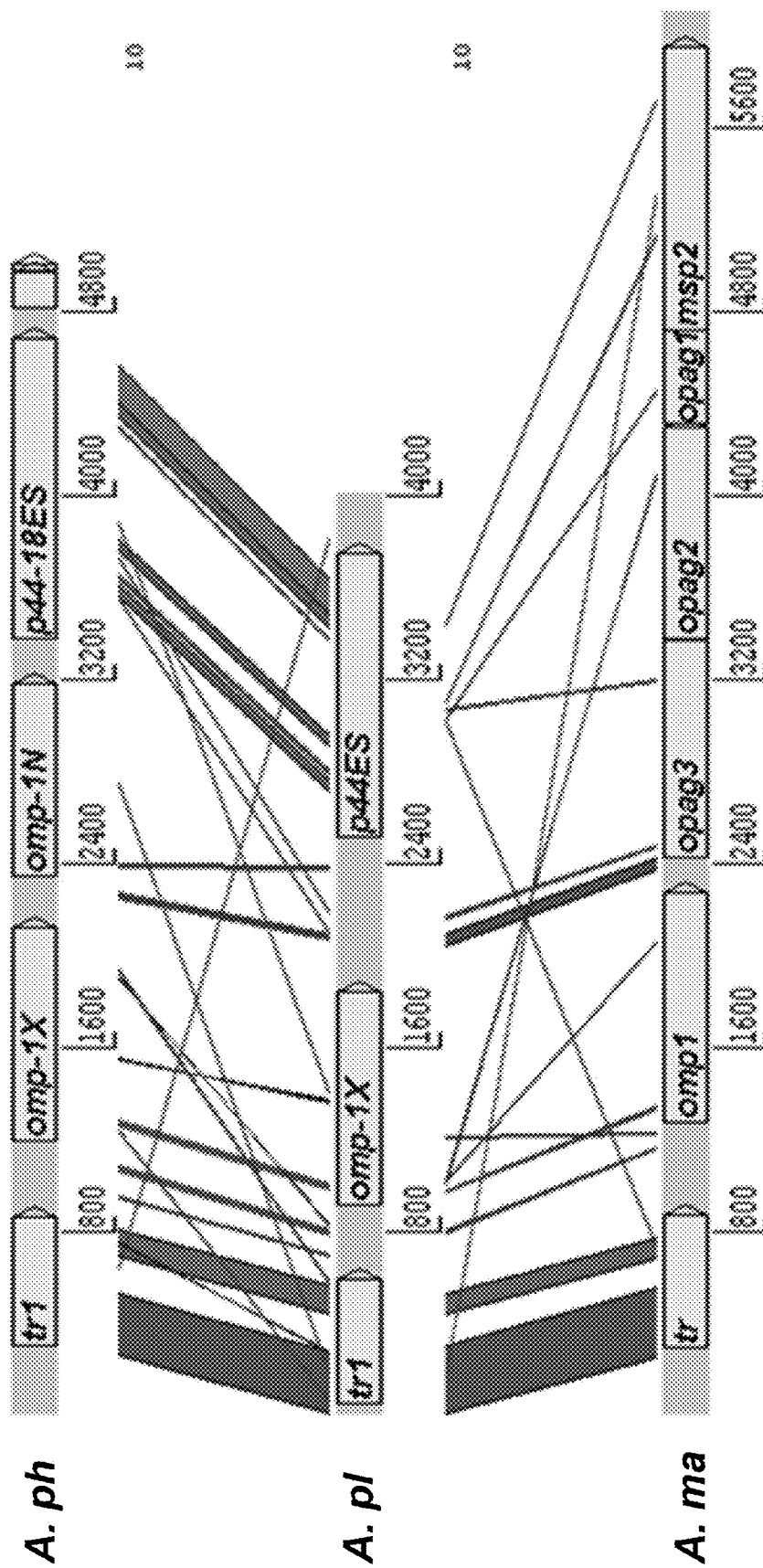


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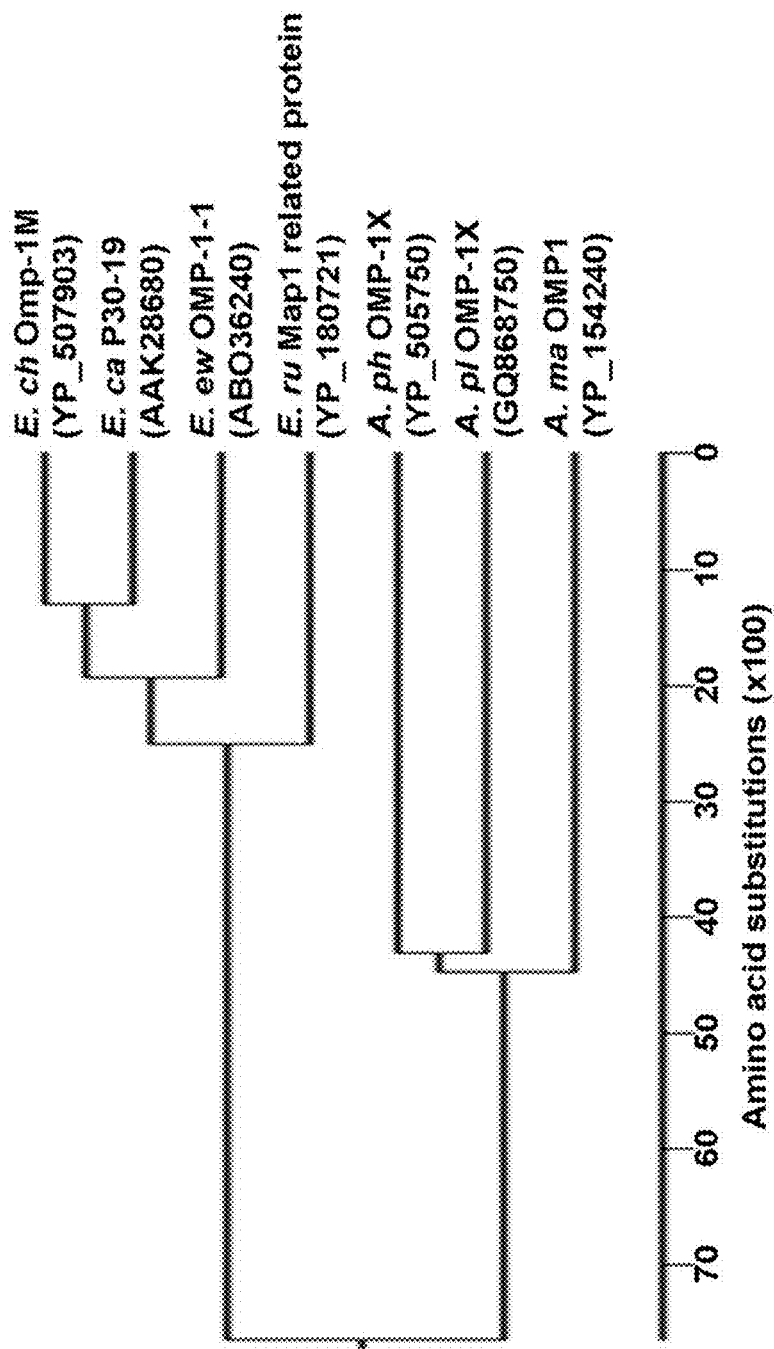


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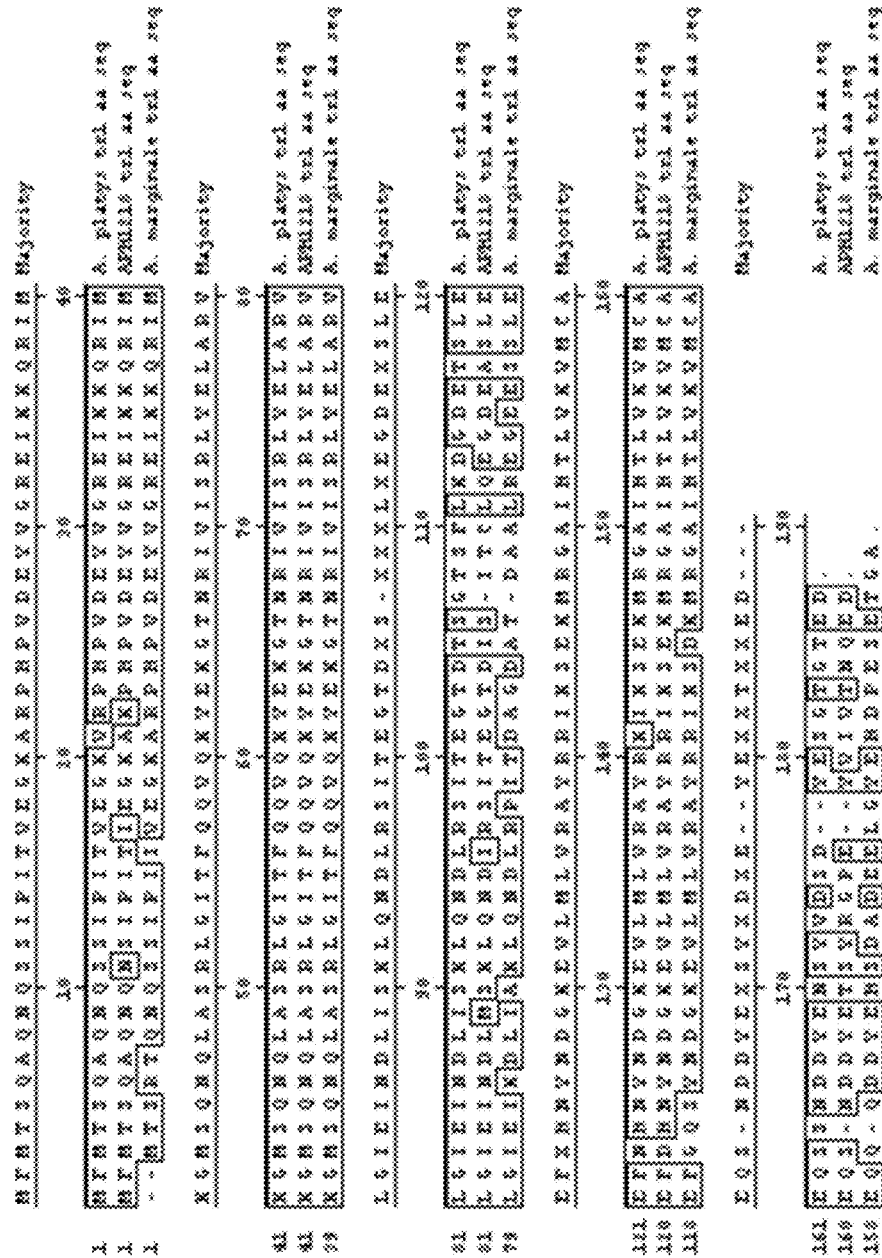
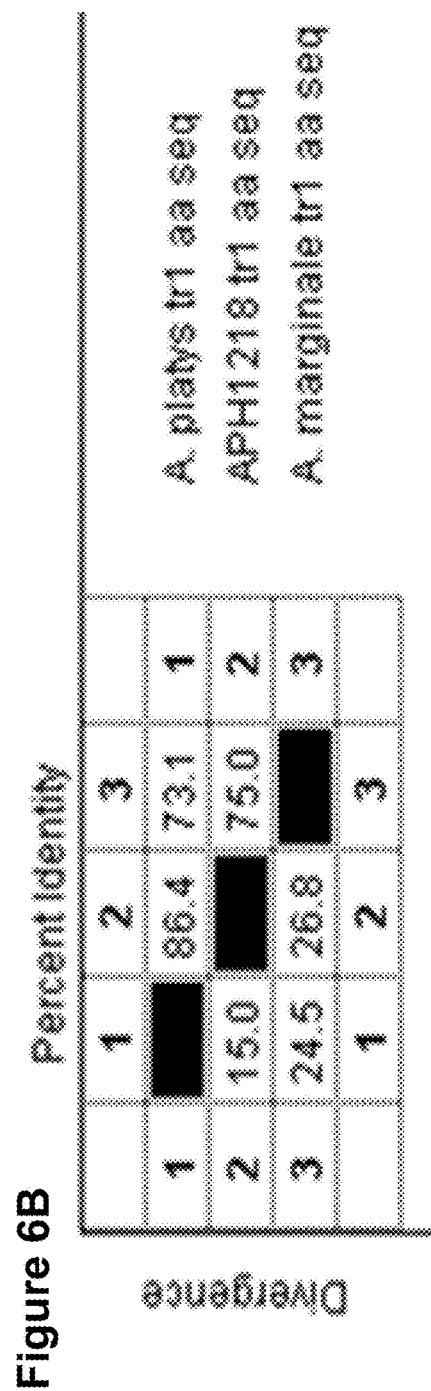
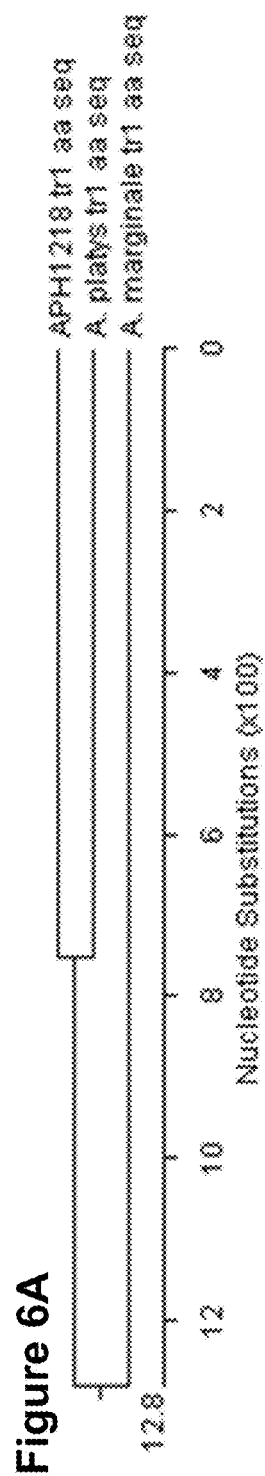
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Figure 5



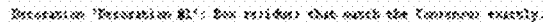


Figure 7

Figure 8A

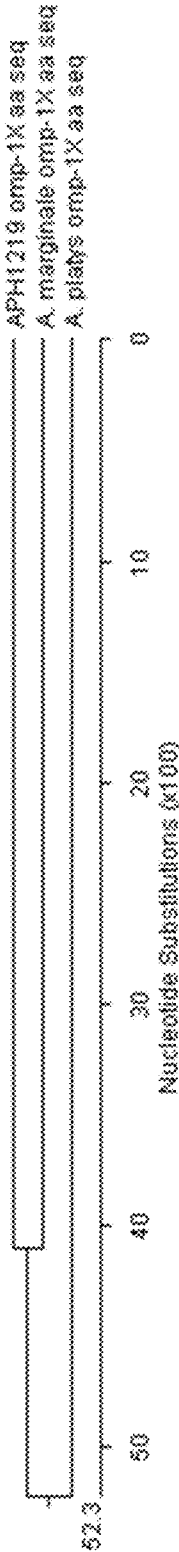


Figure 8B

Percent Identity		Divergence		
	1	2	3	
1		42.3	39.5	1
2	96.5		45.3	2
3	112.7	82.1		3
	1	2	3	
A. platys omp-1X aa seq				
APH1219 omp-1X aa seq				
A. marginale omp-1X aa seq				

Deletion: 'Deletion #1': Two residues that match the consensus exactly.

Figure 9

Figure 10A

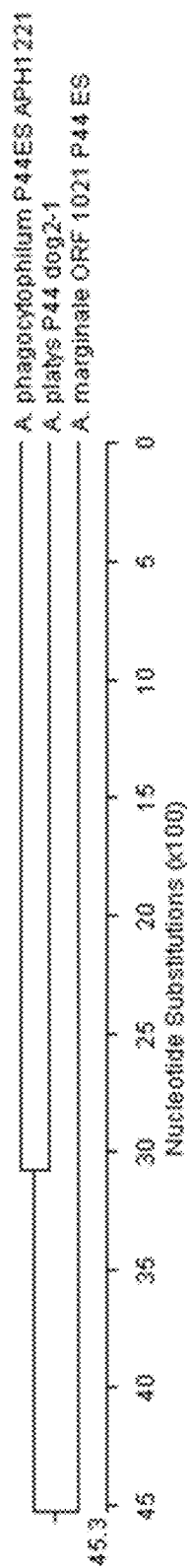


Figure 10B

Percent Identity		Divergence		
	1	2	3	
1		46.1	41.4	A. marginale ORF 1021 P44
2	81.9		51.9	A. phagocytophilum P44ES
3	99.4	61.5		A. platys P44 dog2-1
	1	2	3	

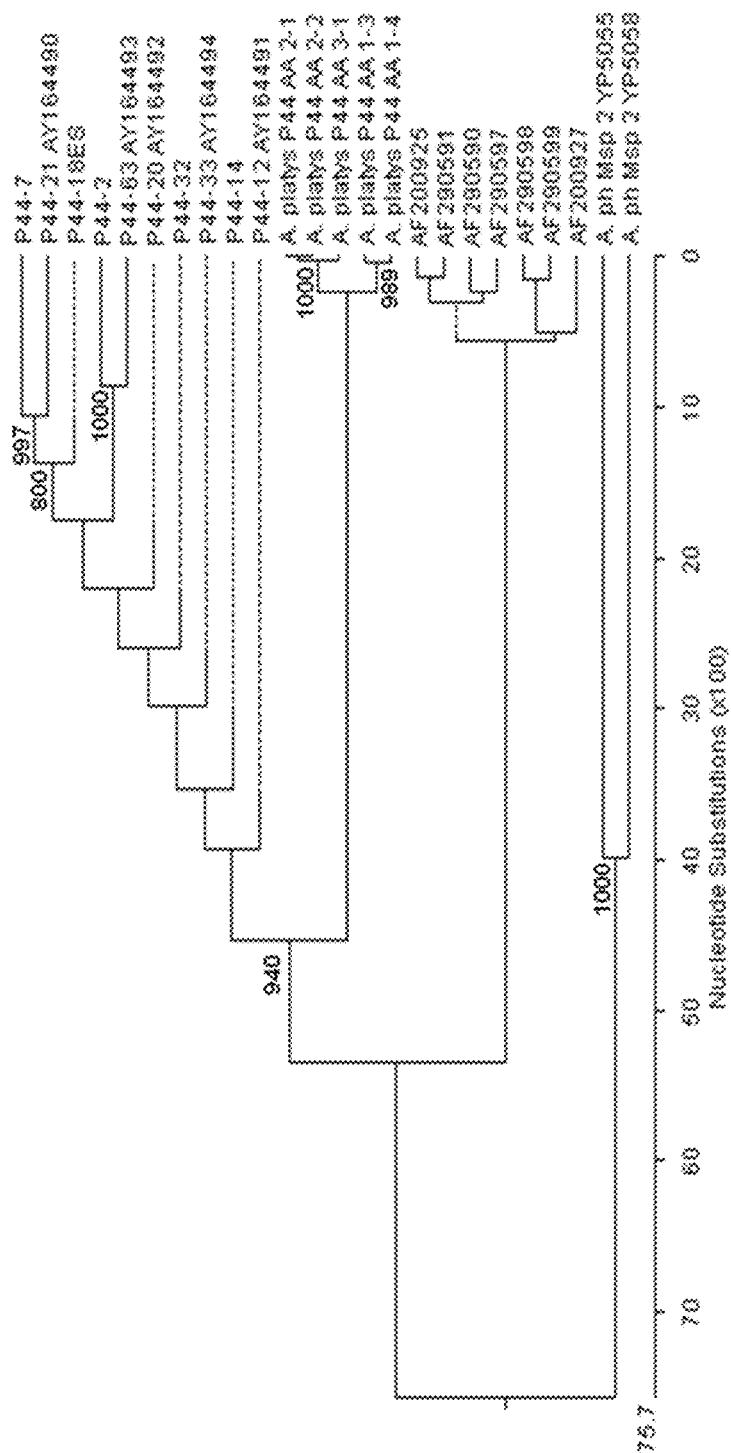


Figure 11

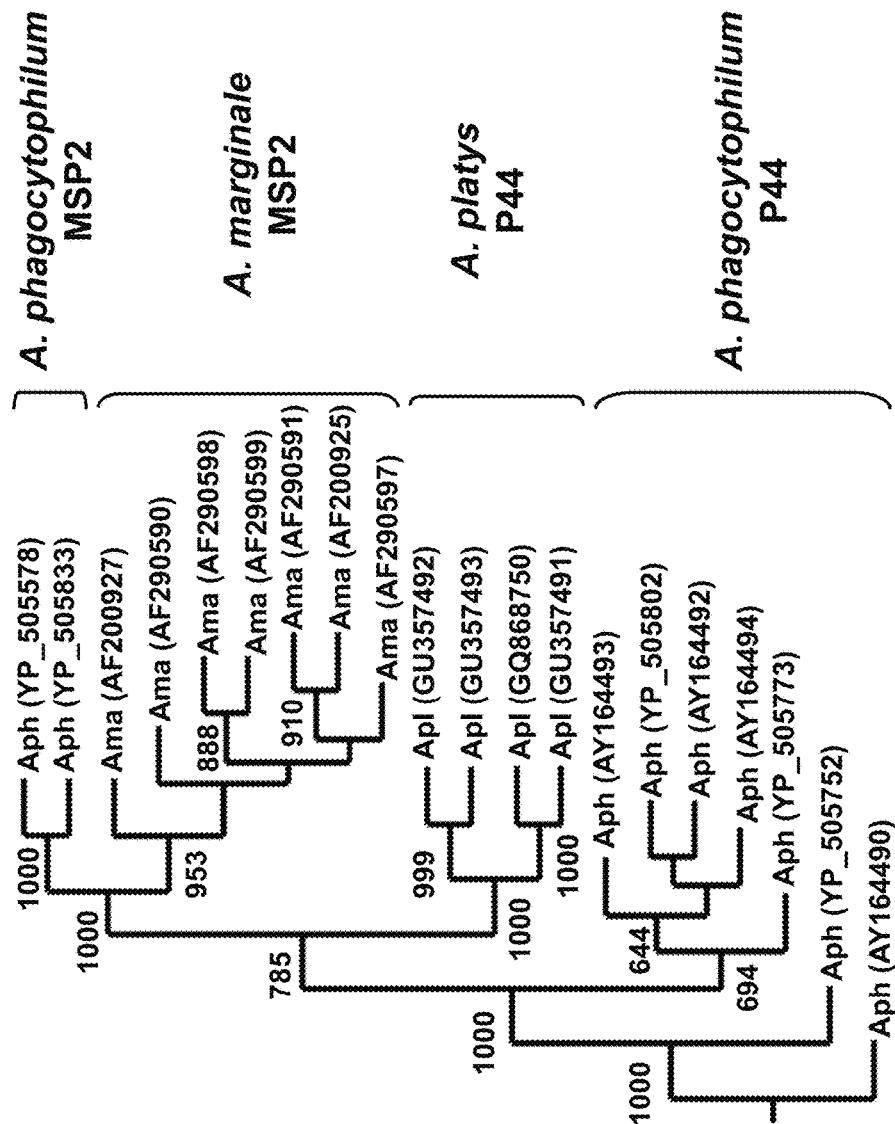
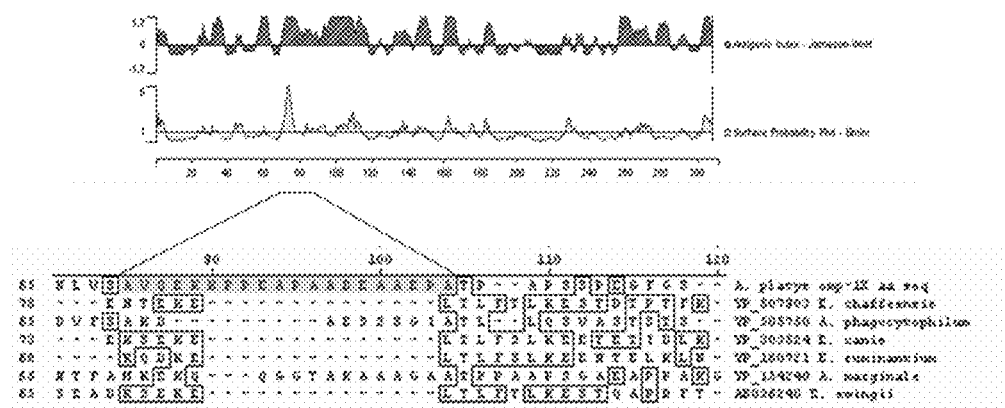


Figure 12

A. platys Omp-1x



A. Platys P44ES

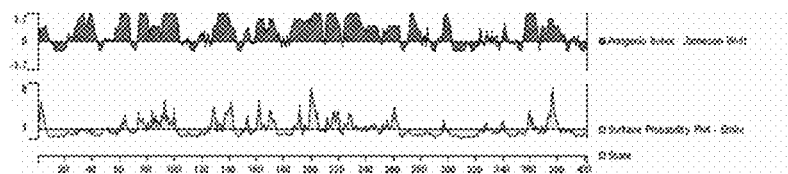
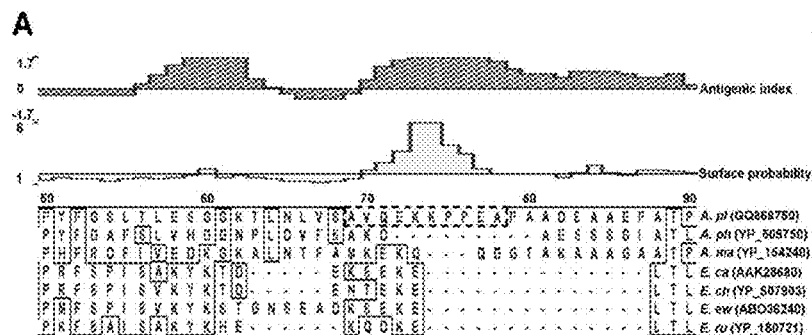


Figure 13B



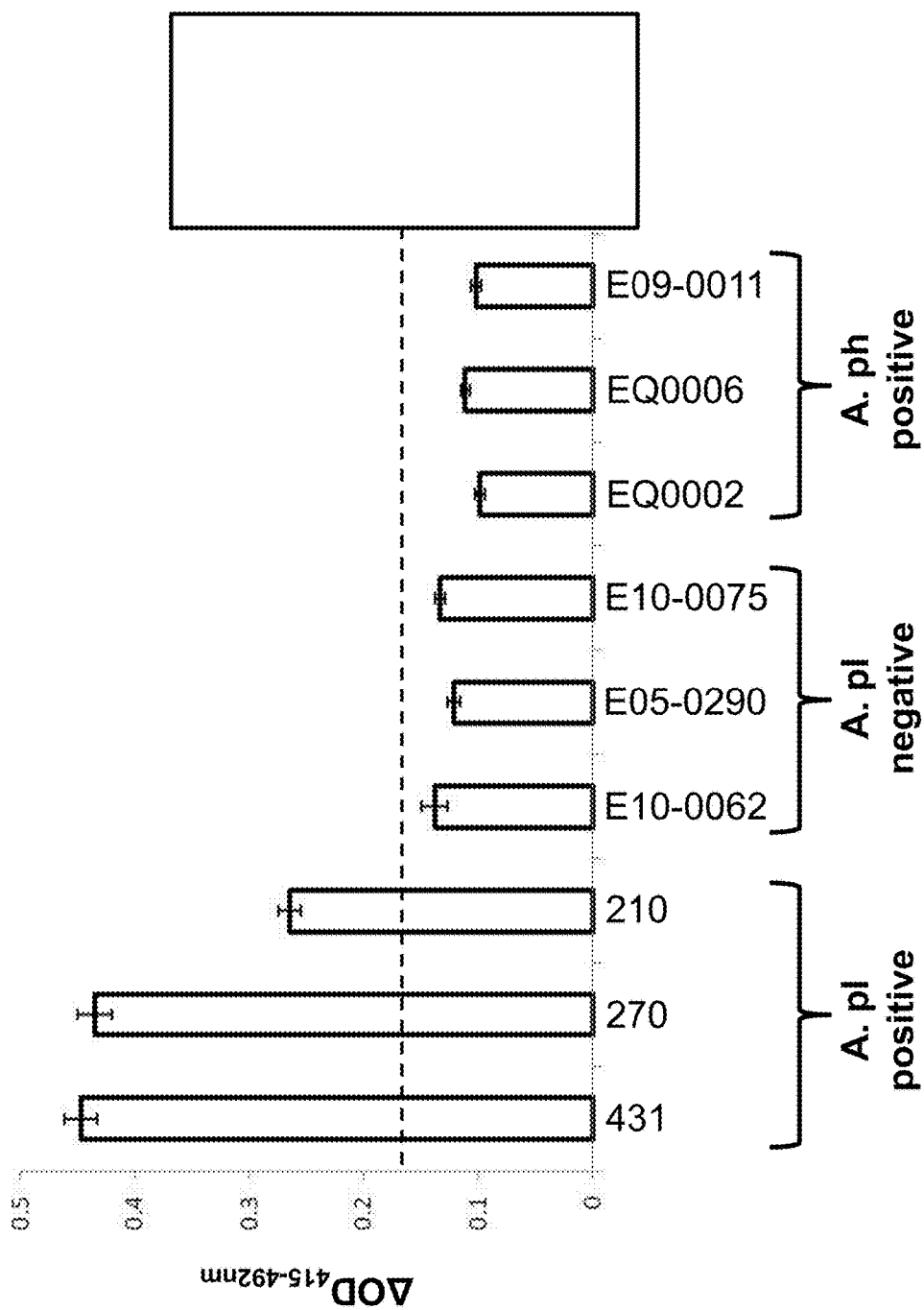


Figure 14

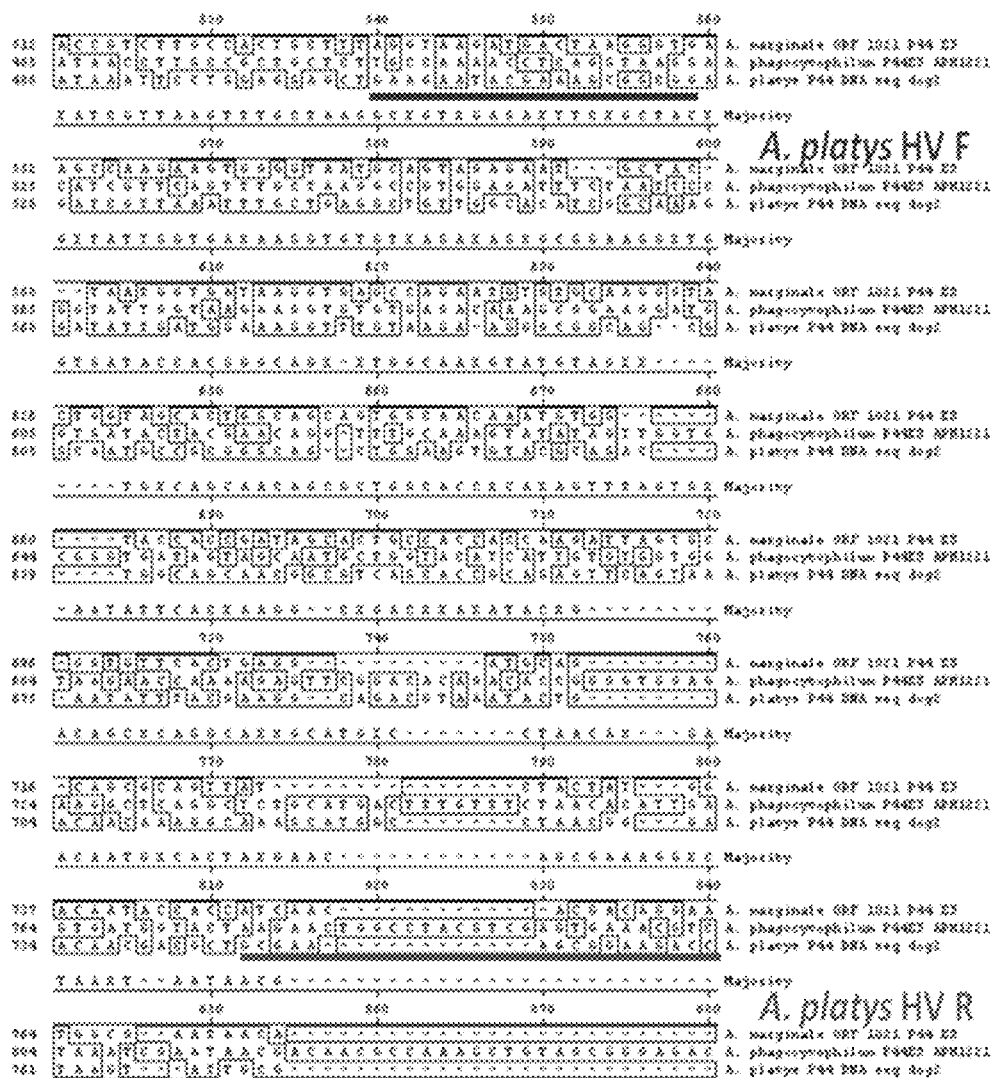


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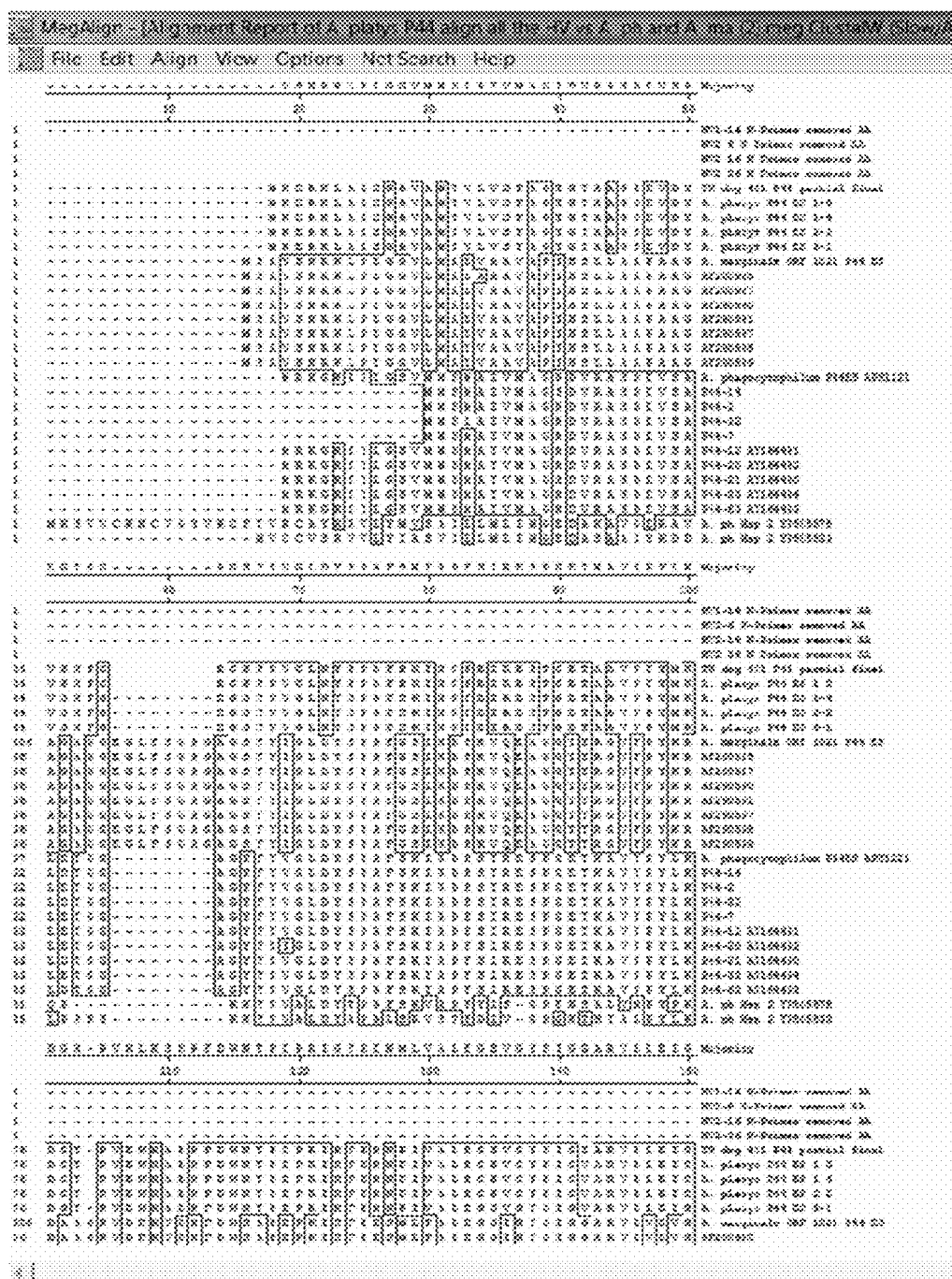


Figure 16

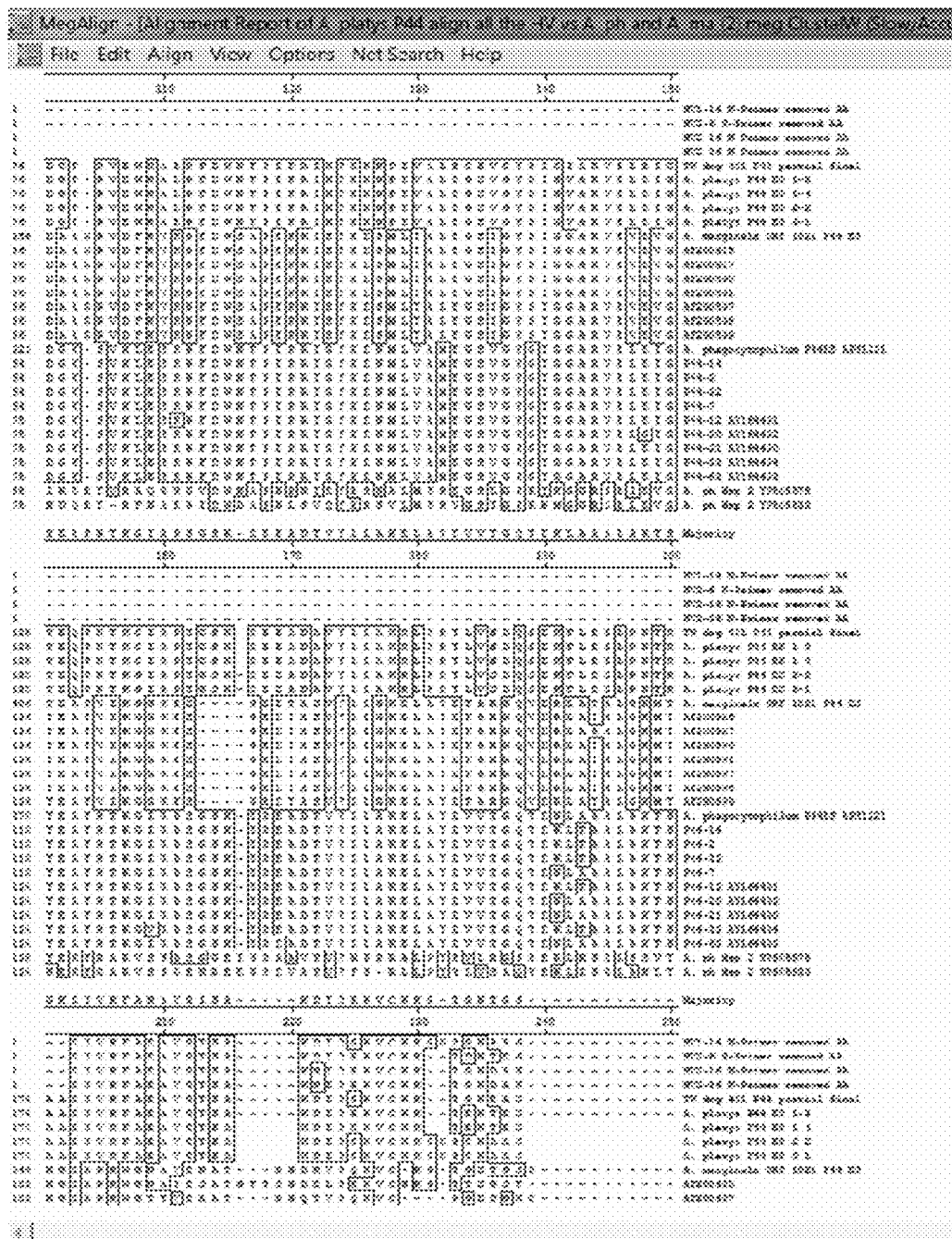


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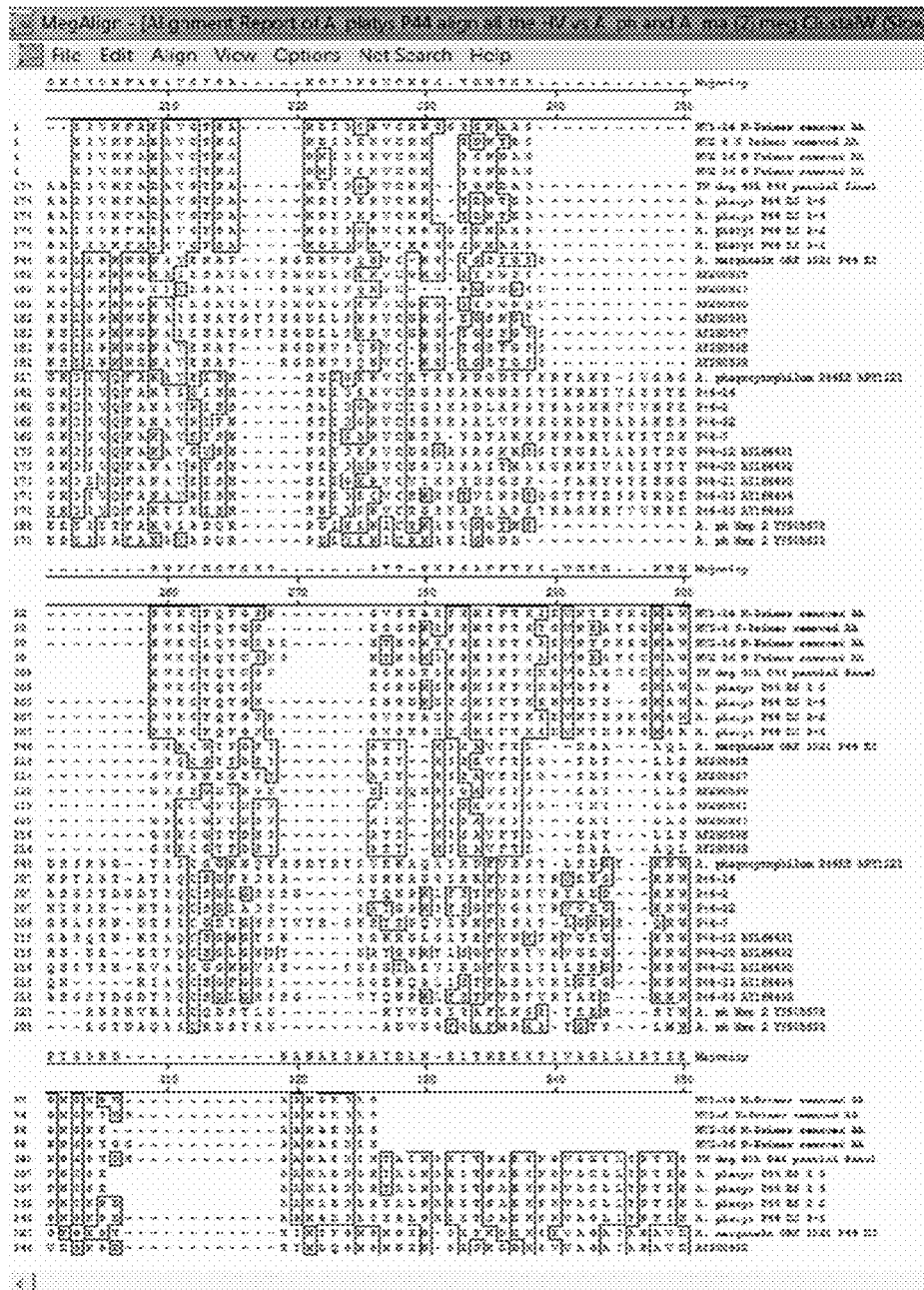
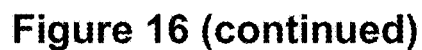


Figure 16 (continued)



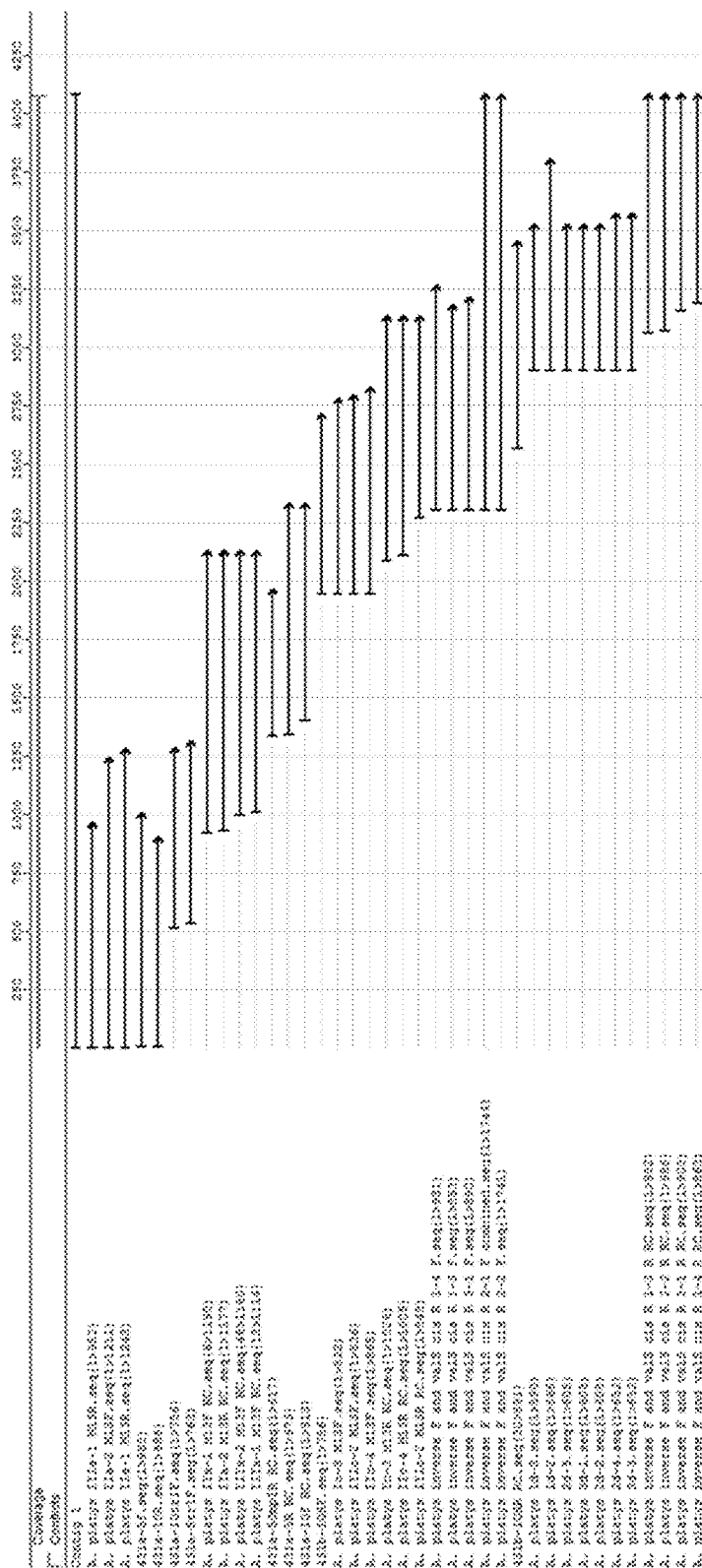


Figure 17

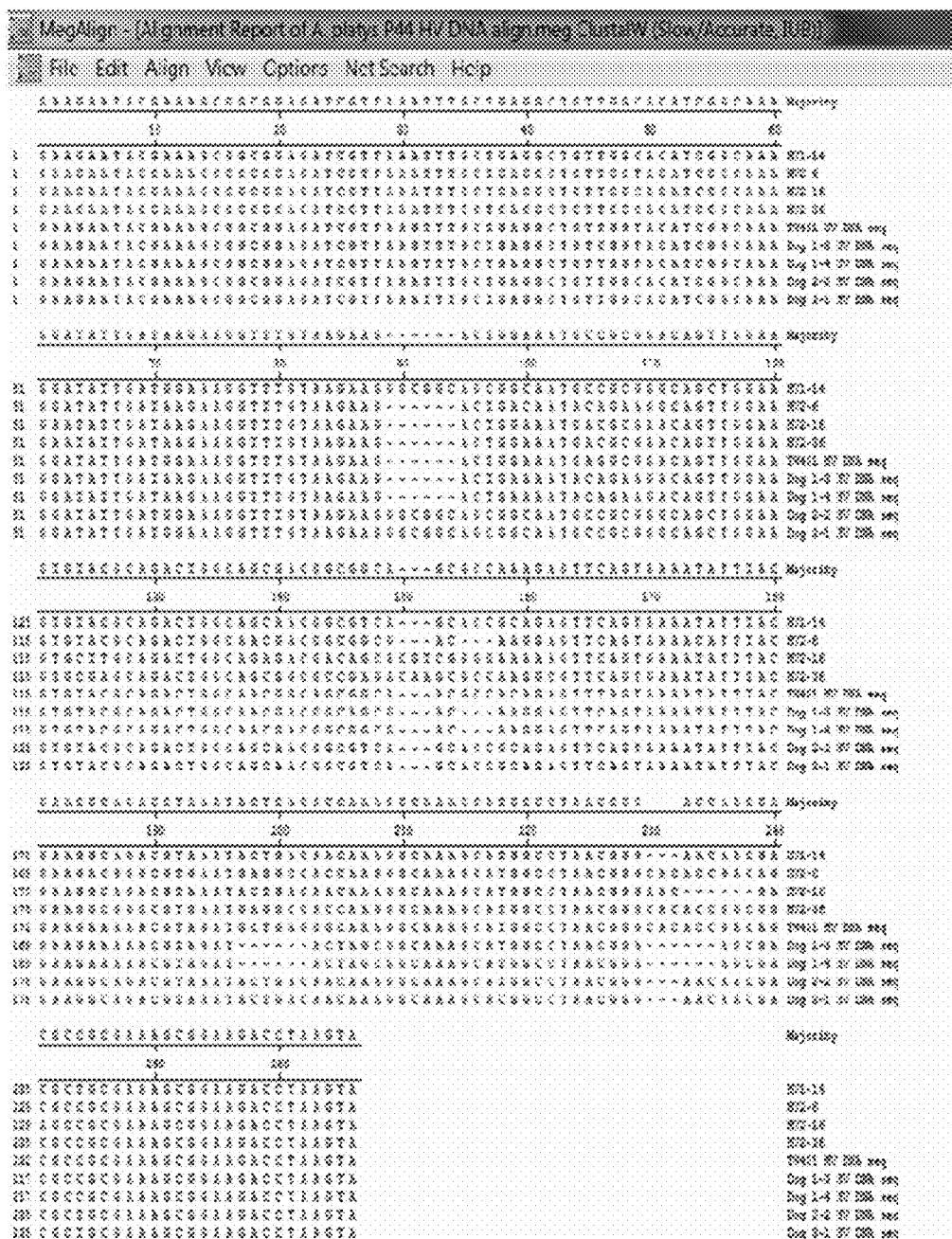


Figure 18

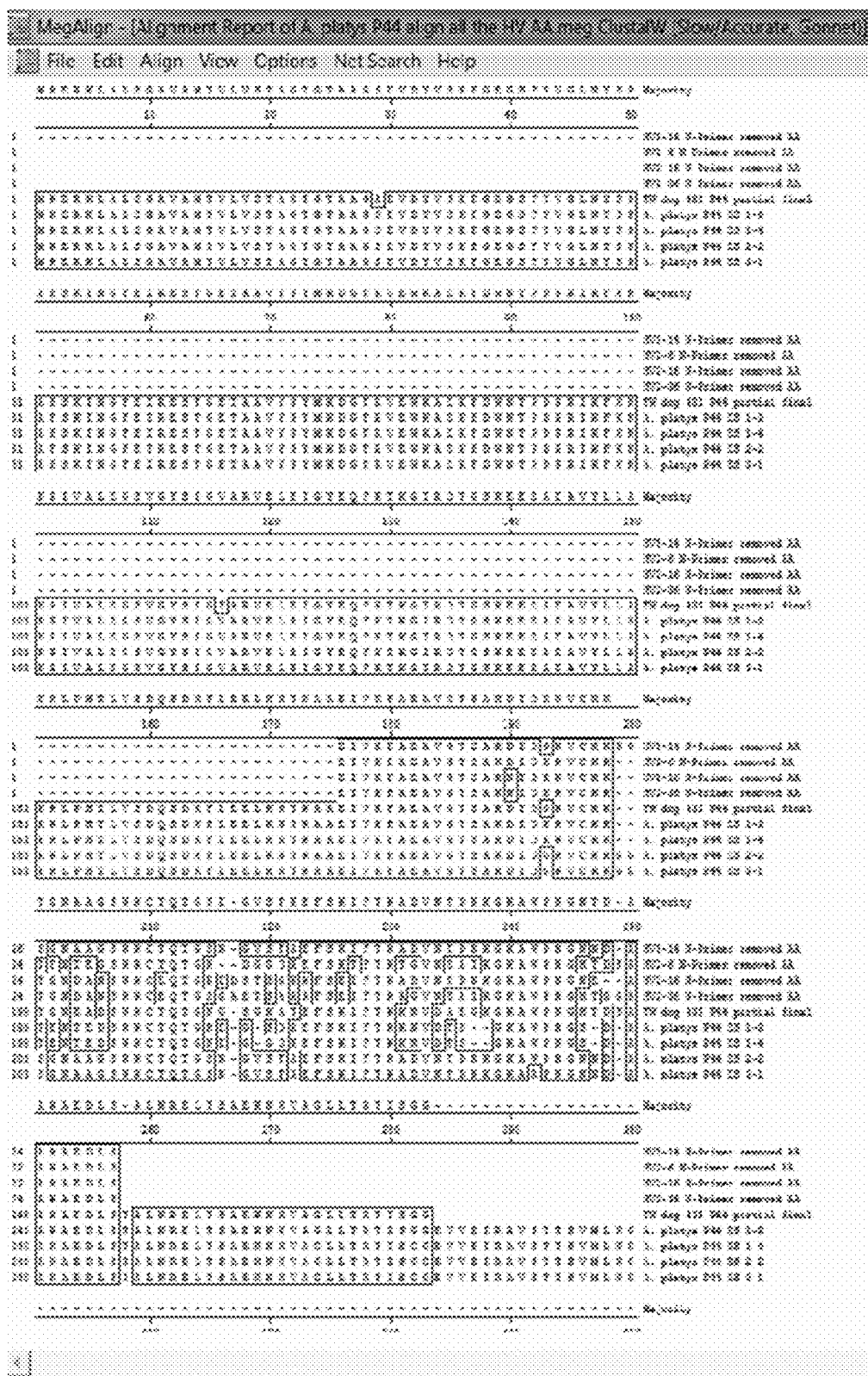
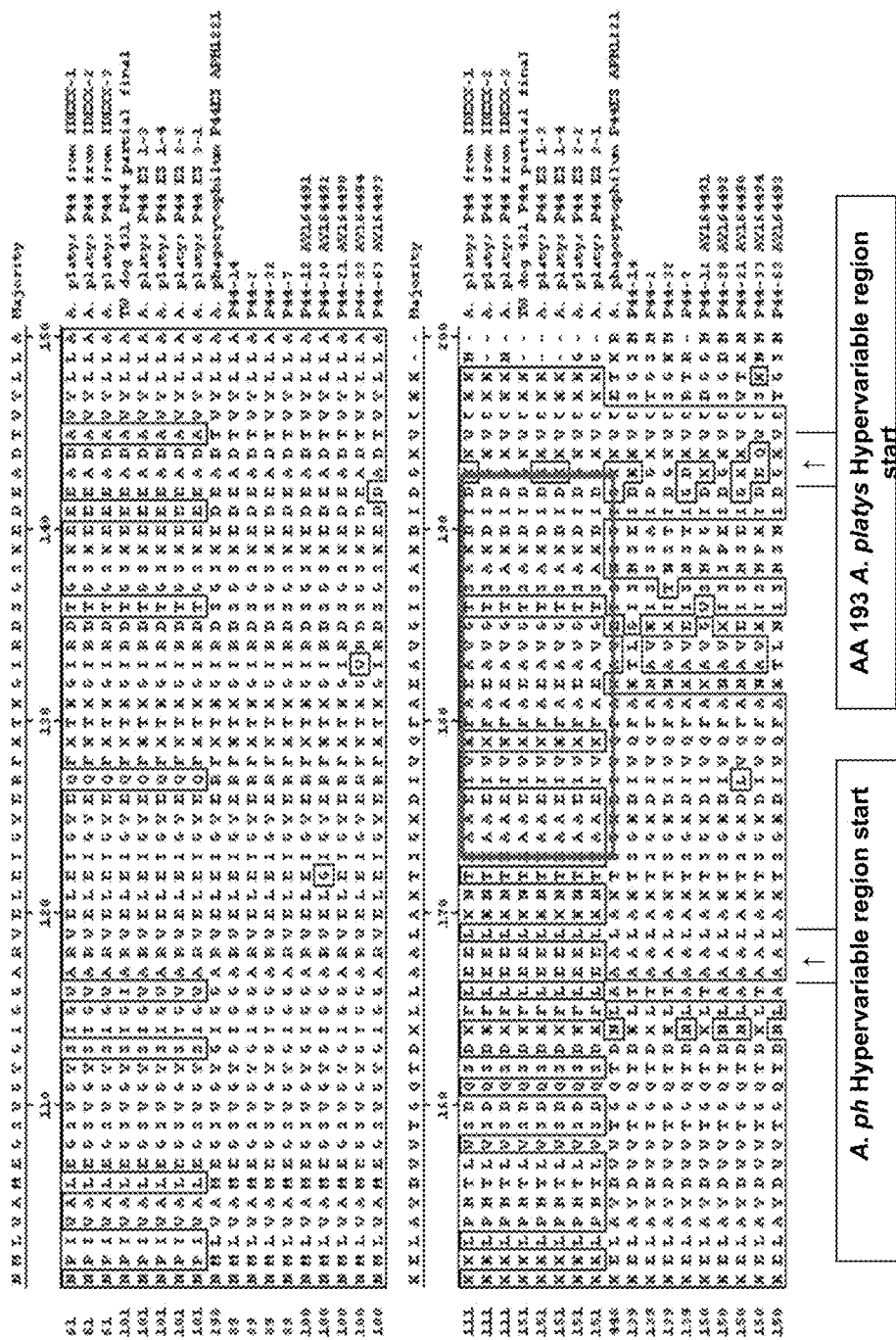
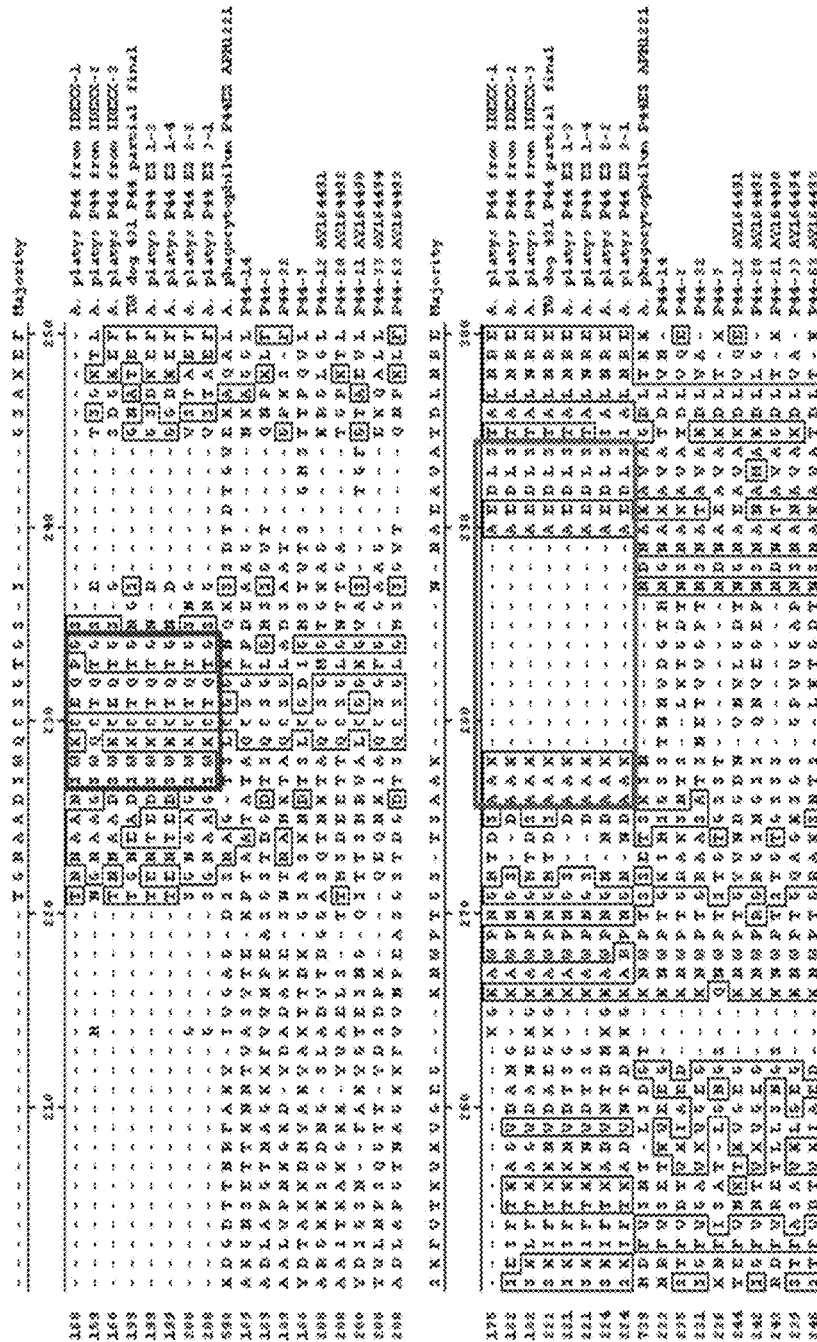


Figure 18 (continued)

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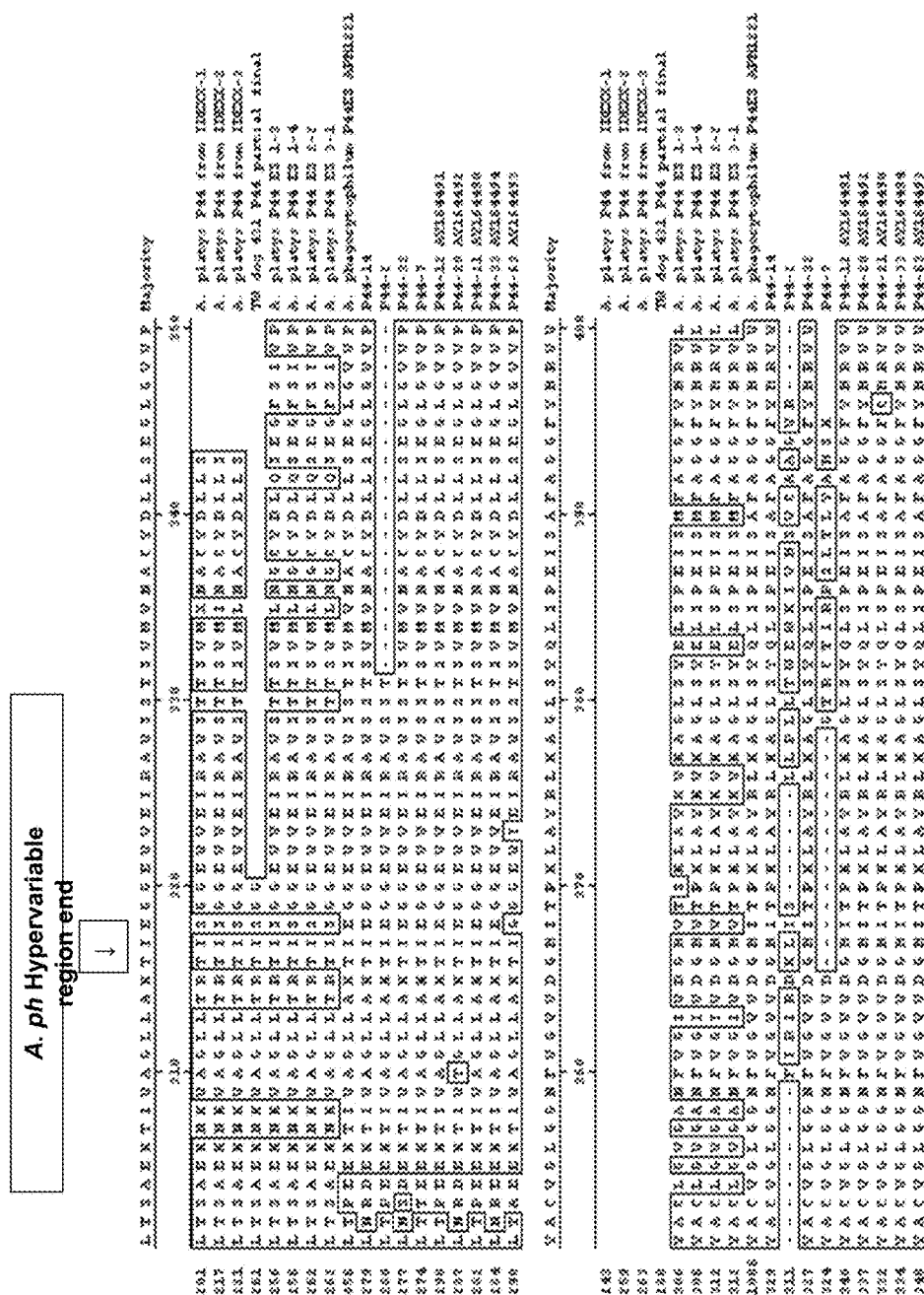
Figure 19





AA 247 *A. platys*
Hypervariable region end

Figure 19 (continued)



[illegible]

Figure 19 (continued)



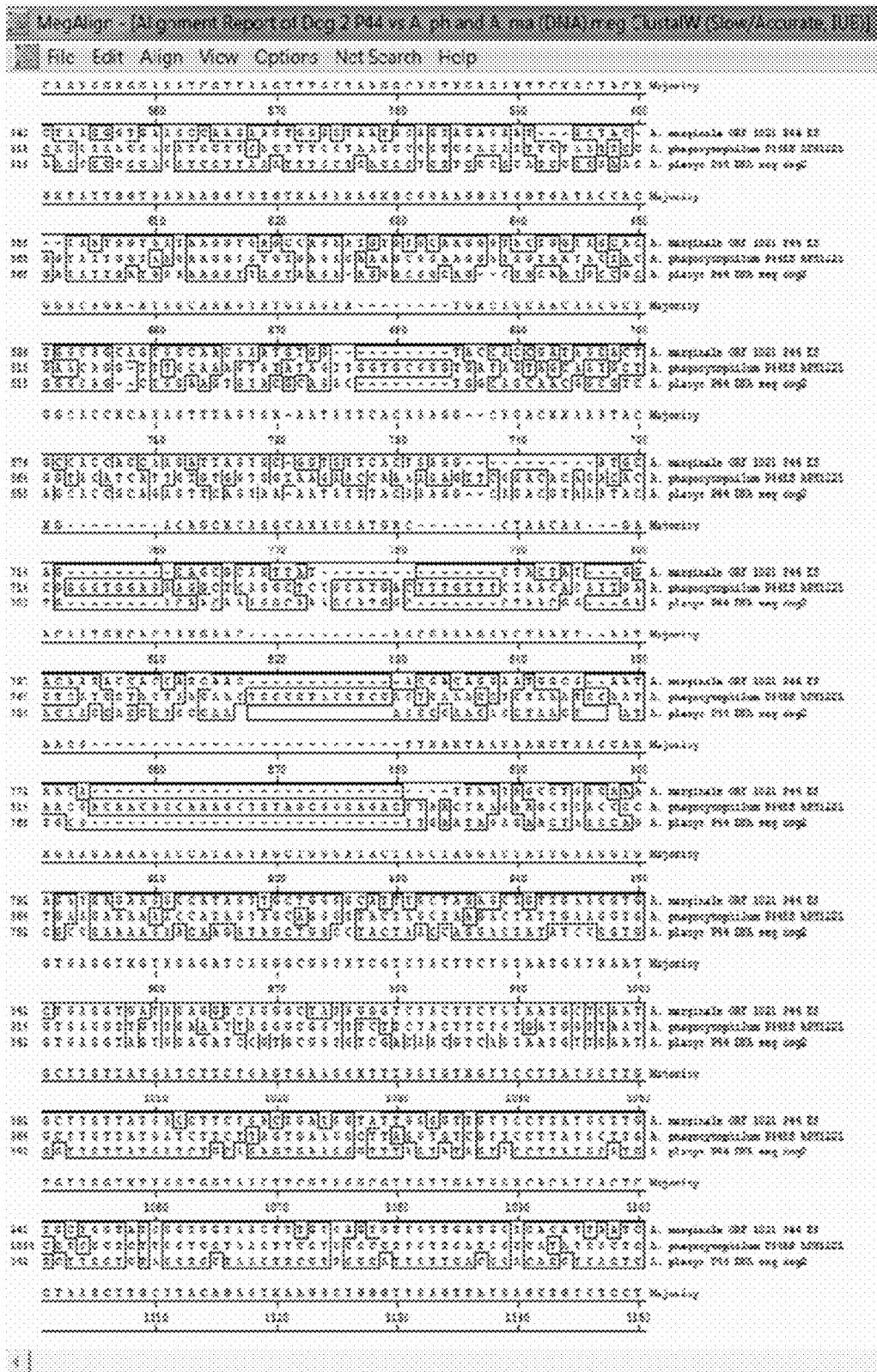




Figure 20 (continued)

Redacted Visual Cloning
A platys P44 complete from dog2



Figure 21

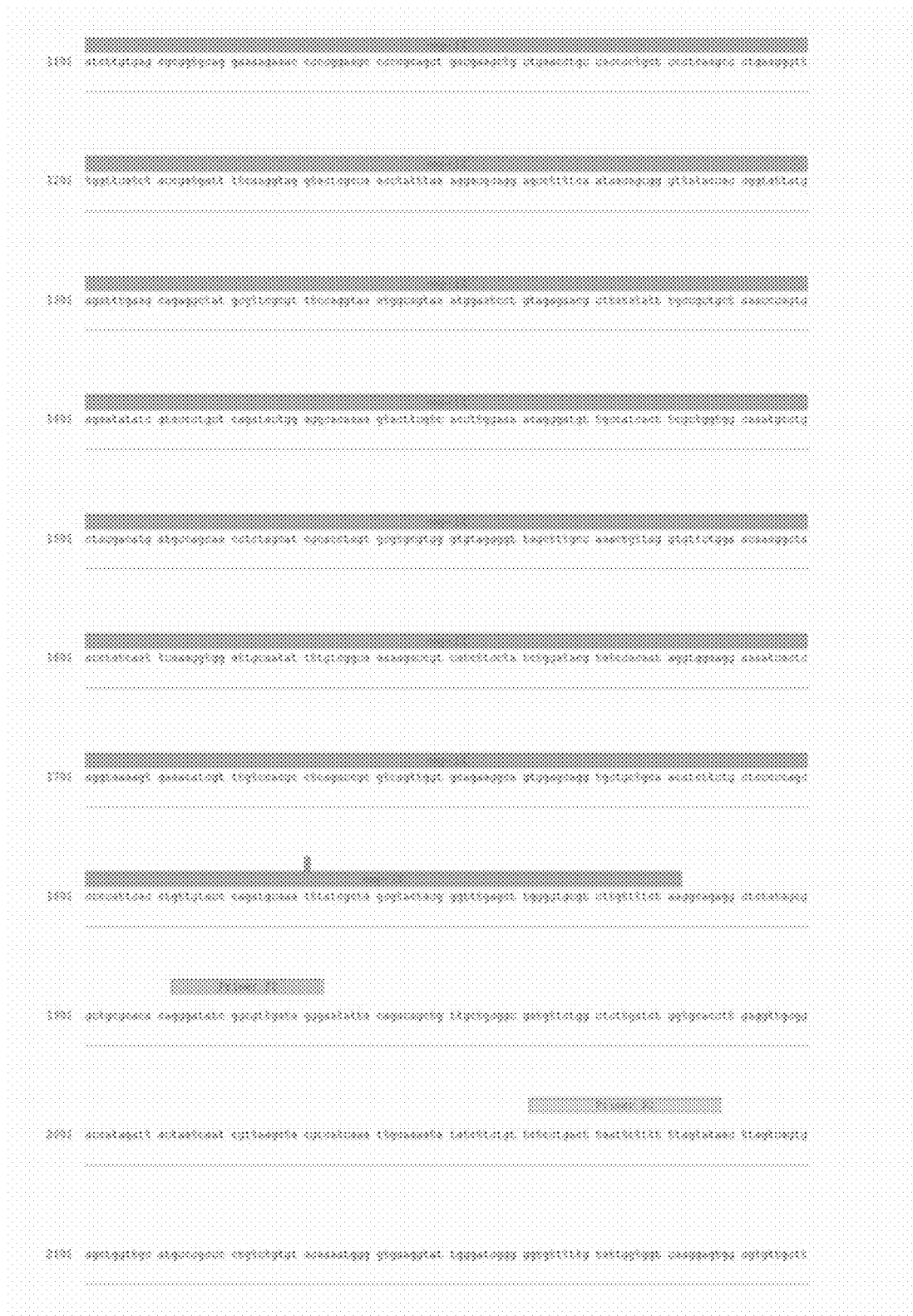


Figure 21 (continued)



Figure 21 (continued)

A. platys Omp1-x

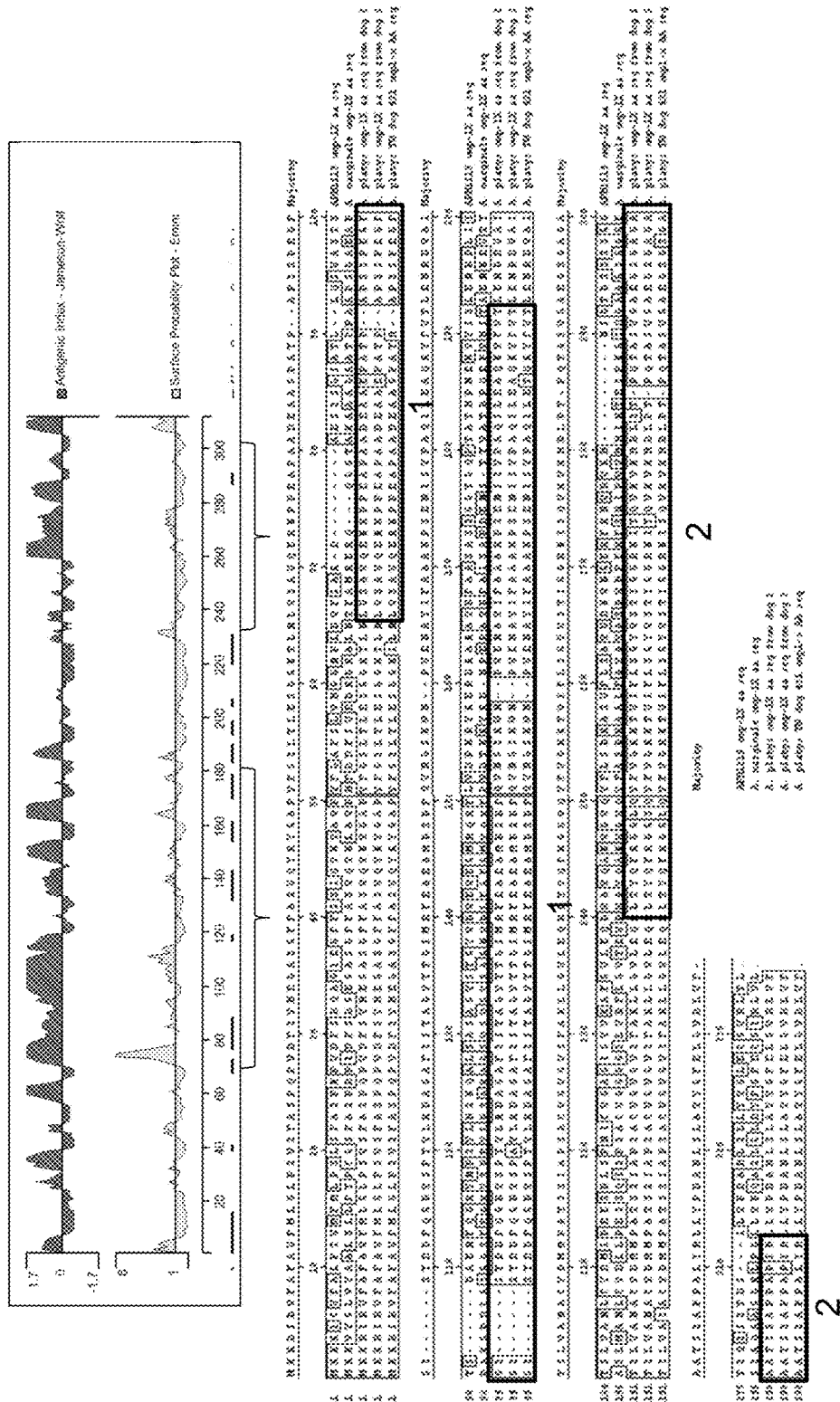


Figure 22

A. platys P44ES

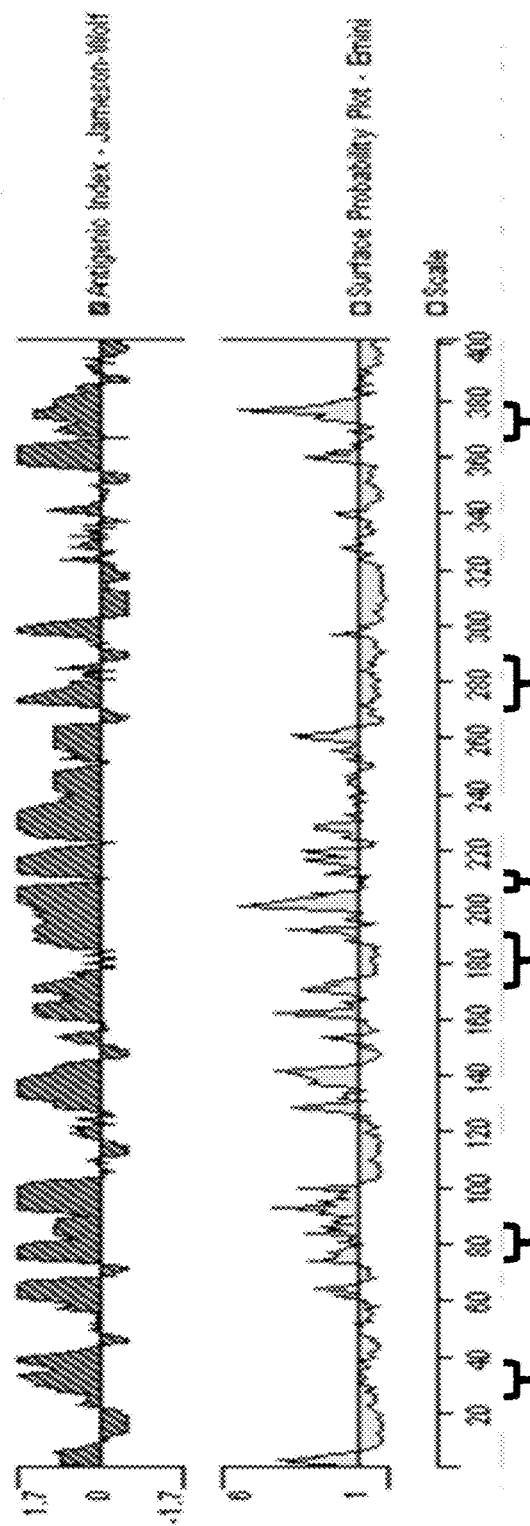


Figure 23

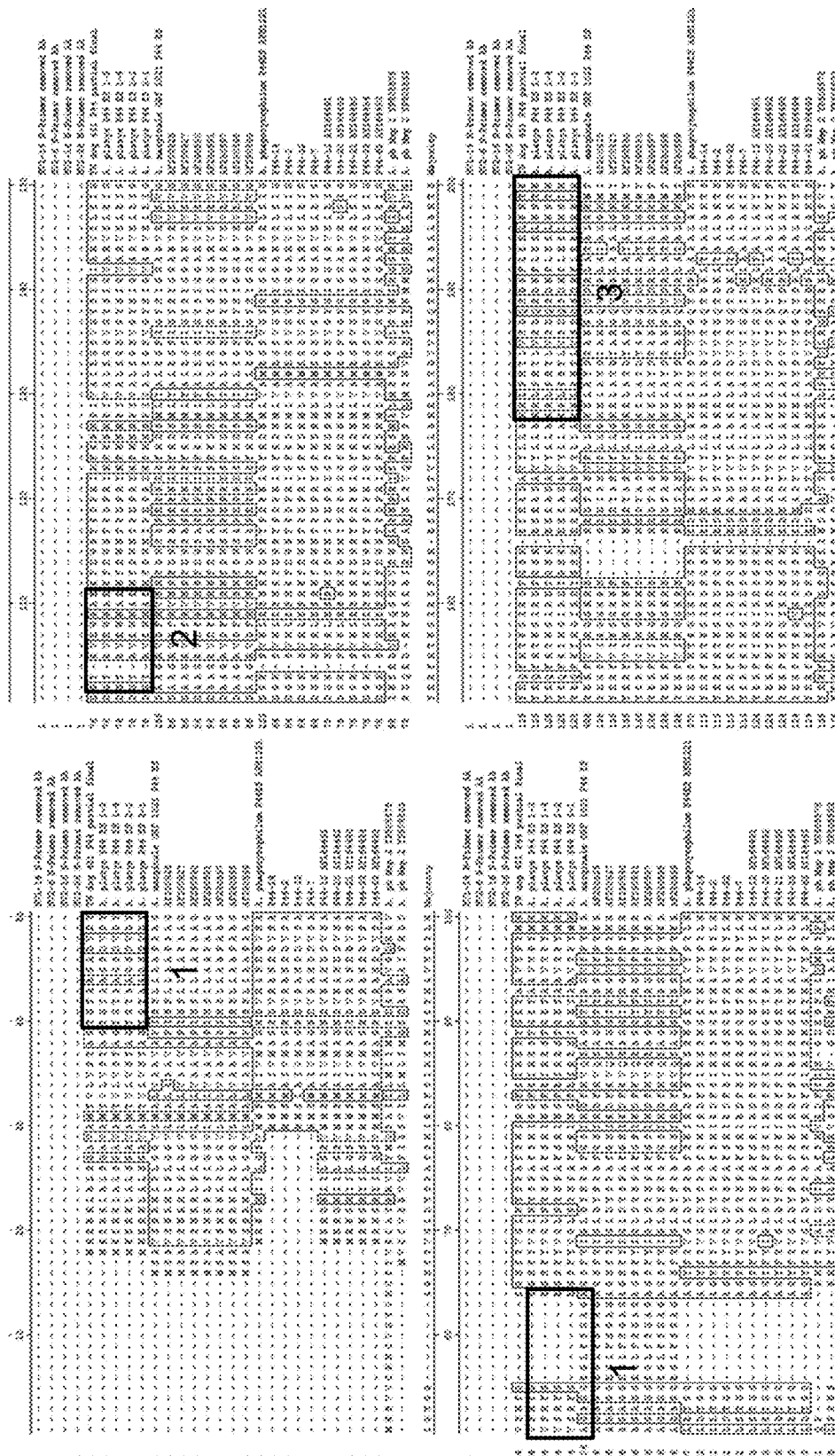


Figure 23 (continued)

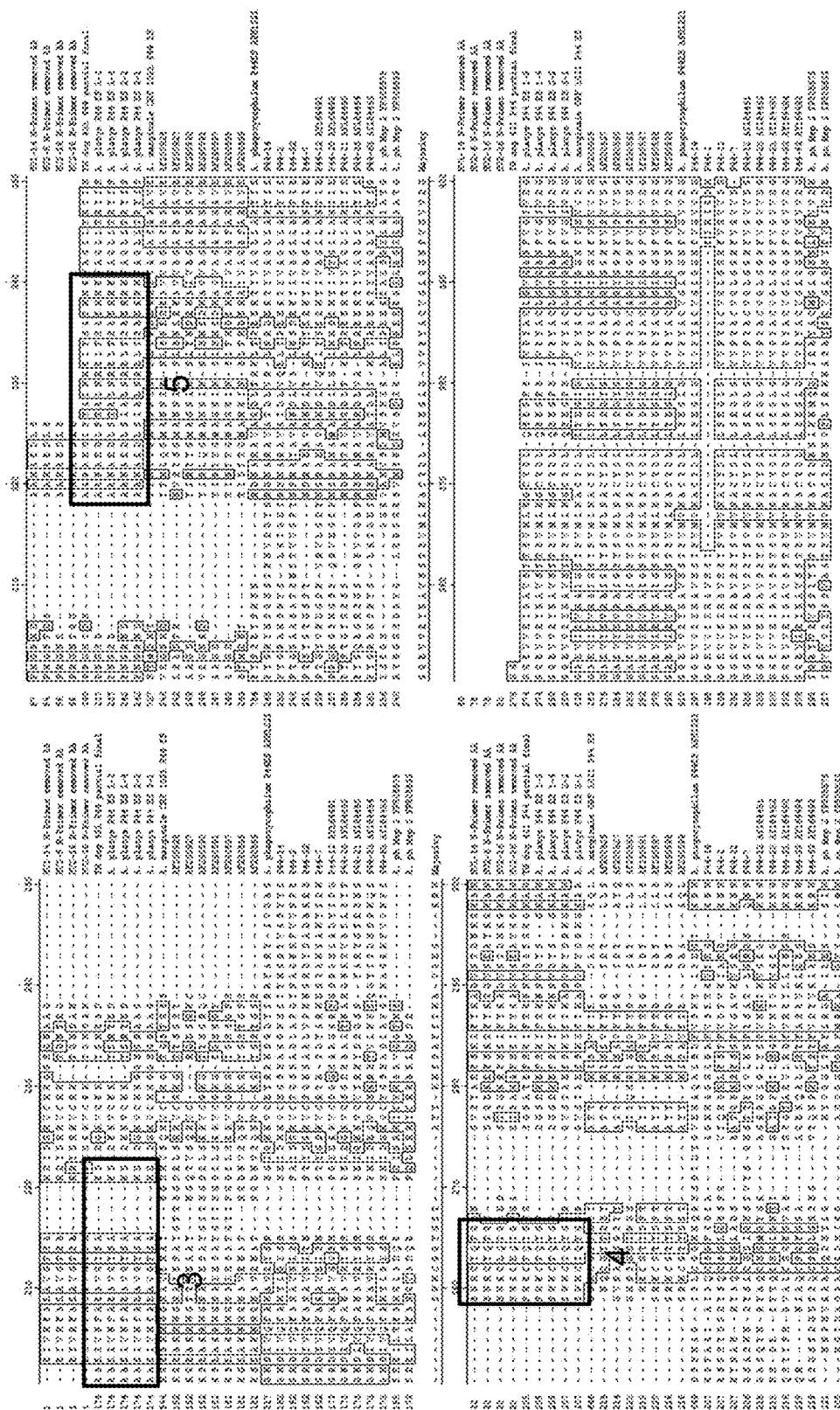


Figure 23 (continued)

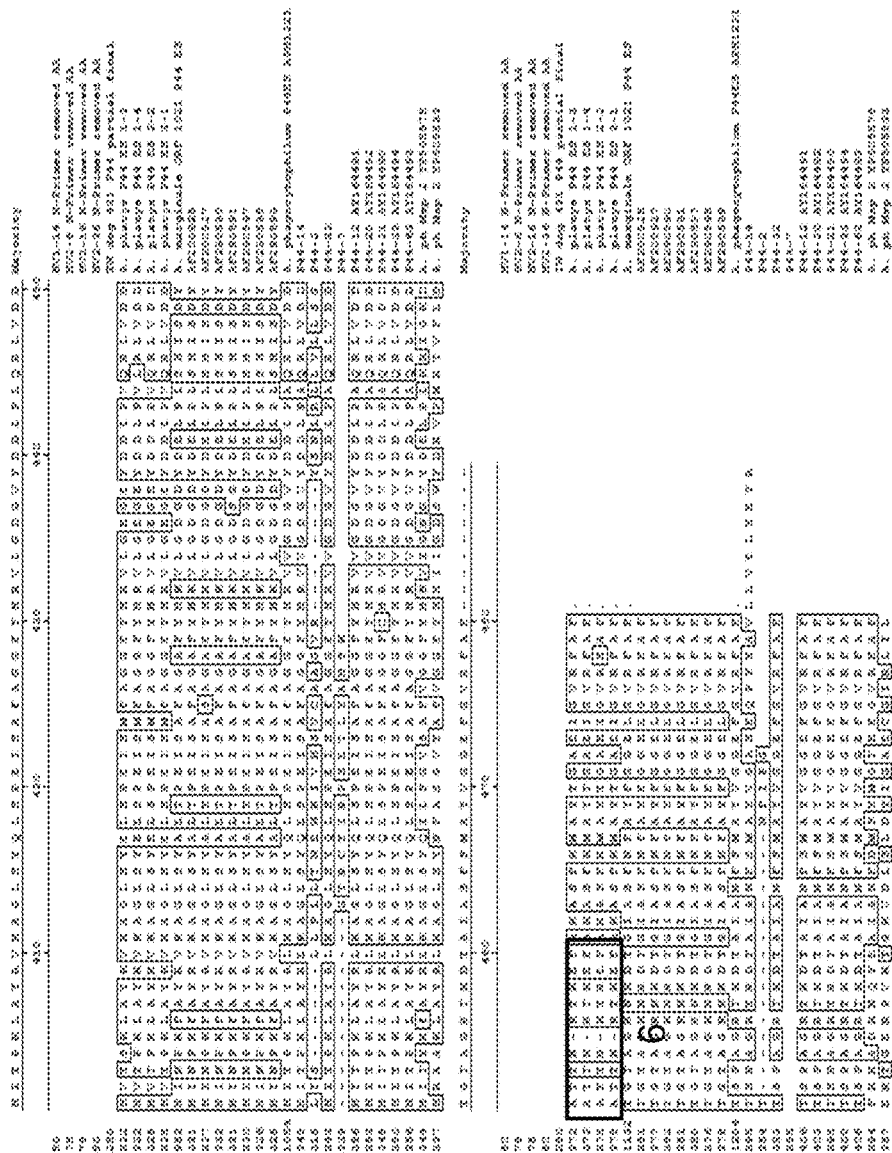


Figure 23 (continued)

1. The first group of students (Group A) was assigned to read the text and identify the main idea of the passage. They were then asked to write a short paragraph summarizing the main idea in their own words.

1

COMPOSITIONS AND METHODS FOR THE
DETECTION OF *ANAPLASMA PLATYS*

GOVERNMENT RIGHTS

This invention was made with government support under R01 AI47885 and R01 AI054476 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND

Anaplasma platys (formerly *Ehrlichia platys*), an obligatory intracellular bacterium, was first described as a rickettsia-like agent in the platelets of dogs from Florida with infectious canine cyclic thrombocytopenia (ICCT) in 1978.²⁵ Authors pointed out morphological and biological similarity of this bacterium to *Ehrlichia canis* in infected dogs and *Anaplasma marginate* in infected cattle, two members of the family Anaplasmataceae,²⁵ which were well-known at that time. Clinical signs of ICCT are fever, depression, appetite loss, anorexia, and bleeding tendencies.²² Parasitemia and thrombocytopenia occur in cycles at approximately 10 to 14 day intervals.²² *Anaplasma platys* responds well to doxycycline, a tetracycline antibiotic, as the primary means of treatment.

Based on indirect fluorescence antibody (IFA) tests using the platelet-rich plasma from a dog experimentally infected with ICCT, minimal serologic cross-reaction was found to occur between *A. platys* and *E. canis*, and the researchers proposed the name "*Ehrlichia platys*" for this bacterium.²² In 1992, the 16S rRNA gene sequence of *A. platys* was reported.³ Subsequently, the groEL gene sequence of *A. platys* was disclosed.^{29, 67} Phylogenetic analysis of these sequences showed that this is a distinct bacterium closely related to *Anaplasma phagocytophilum* and *Anaplasma marginate*, which led to reclassification of this bacterium into the genus *Anaplasma*.¹⁷ Later it was reported that although *A. platys* does not cross-react with serum antibodies from dogs infected with *E. canis* on IFA tests, the *A. platys* antigen cross-reacts with anti-*Anaplasma phagocytophilum* antibodies.³²

Seropositive dogs have been found in Florida, Pennsylvania, Texas, Louisiana, Illinois, California, Arkansas, Mississippi, Idaho, and North Carolina. High rates of *A. platys* and *E. canis* dual positive dogs have also been reported throughout these areas.²² *A. platys* DNA has also been detected in dogs throughout Brazil,²⁰ Greece,⁴³ France,³³ Taiwan,¹⁵ Spain,⁵⁴ China,²⁸ Australia,¹² Portugal,¹³ the Democratic Republic of Congo,⁵⁵ Japan,⁶¹ Thailand,²⁹ and Venezuela.⁵⁹ It is believed that the brown dog tick, *Rhipicephalus sanguineus*, is the biological vector which transfers *A. platys* to potential hosts. In fact, *A. platys* has been detected in brown dog ticks in Okinawa, Japan,³⁴ Spain,⁵⁸ and the Democratic Republic of Congo.⁵⁵ However, it has not been experimentally proven that *R. sanguineus* is the biological vector responsible for the transfer of *A. platys*.⁵⁶ To date, *A. platys* has never been culture isolated. Consequently this bacterium is poorly understood at the molecular, cellular, or immunologic level, and to date, no antigen has been identified for this bacterium.

In *A. phagocytophilum* and *A. marginate*, surface-exposed immunodominant 44 kDa major outer membrane proteins (P44s/Msp2s) are encoded by the p44 (msp2) polymorphic multigene family.^{6, 9, 39, 41, 69-71} In *A. phagocytophilum*, P44 proteins consist of a single central hypervariable region of approximately 94 amino acid residues and an N-terminal

2

and C-terminal conserved regions of approximately 186 and 146 amino acid residues, respectively.⁴¹ A single polymorphic p44/msp2 expression locus (p44/msp2ES) is found in the genome of *A. phagocytophilum*¹⁰ and *A. marginate*,²⁶ respectively. Both expression loci are found downstream of tr1 genes encoding putative transcriptional factor and homologs of *Ehrlichia chaffeensis* omp-1 genes encoding polymorphic major outer membrane protein (MOMP).^{6, 8, 39} At p44/msp2ES, p44s and msp2 donor sequences elsewhere in the genome undergo recombination via RecF pathway to allow variable p44/msp2ES expression under the same promoter.^{6, 8, 39, 40} This mechanism is thought to facilitate P44/Msp2 antigenic variation persistent infection and for adaptation to new environments such as transmission between tick and mammalian hosts.^{7, 11, 38, 40, 65, 71} Purified native P44 from *A. phagocytophilum* and purified native OMP-1s (P28 and OMP-1F) of *Ehrlichia chaffeensis* have porin activity.^{30, 37}

Anaplasma platys (Apl) is an obligate intracellular bacteria that infects platelets and causes a cyclic thrombocytopenia in the dog. The observation that a dog can be affected by this rickettsia agent, and the disease is most likely transmitted by the *Rhipicephalus* spp of ticks. *Anaplasma platys* was first reported in the United States in 1978 and has since been reported in Europe, Asia, South America, the Middle East, Australia, and Africa. Because of the common vector, *Anaplasma platys* infection is often found as a coinfection with *Ehrlichia canis*. The ability of the organism to produce clinical disease in the dog appears to vary with geography, suggesting that strain differences may contribute to virulence. *Anaplasma platys* is related to another *Anaplasma* species known to cause clinical disease in the dog, *Anaplasma phagocytophilum* (Aph).

Current diagnostic tests that attempt to distinguish Aph and *Anaplasma platys* have limited specificity. PCR for Aph and *Anaplasma platys* using 16SrRNA has also had problems with specificity. Therefore, assays for specific detection of *Anaplasma platys* are needed in the art. Additionally, serological tests for *Anaplasma platys* are also needed.

BRIEF DESCRIPTION OF THE SEVERAL
VIEWS OF THE DRAWINGS

FIG. 1A shows the strategy for *A. platys* p44ES cluster sequencing. *A. phagocytophilum* p44ES and *A. marginate* msp2ES were aligned to design primer F1 (targeting tr1/orf3 upstream highly conserved region) and degenerate primers R1 (targeting p44ES/msp2 C-terminal highly conserved region), R2 (targeting conserved intergenetic region between omp-1X/omp4 and omp-1N/omp3), R3 (targeting p44ES/msp2 N-terminal conserved region) and R4 (based on p44ES/msp2ES downstream conserved valS gene). Primers F2 and F3 were designed based on the sequence results. FIG. 1B shows the final sequence (4,009 bp) was assembled with the SeqMan program from the DNASTAR software suite. Genes are represented as boxes with arrows indicating their orientation. FIG. 1C shows the entire expression locus fragment D (arrow) amplified from the dog 2 blood DNA specimen by primers F1 and R5.

FIG. 2 depicts the synteny analysis, using the Artemis comparison tool, of the *A. platys* (*A. pl*) p44ES cluster relative to *A. phagocytophilum* (*A. ph*) and *A. marginate* (*A. ma*). Each bar corresponds to a good match. Numbers indicate bp. Score cutoffs: 140.

FIG. 3 depicts the synteny analysis, using the Artemis comparison tool, of the *A. platys* (*A. pl*) p44ES cluster relative to *A. phagocytophilum* (*A. ph*) and *A. marginate* (*A.*

ma). Each bar corresponds to a good match. Numbers indicate bp. Score cutoffs: 140 using the Artemis Comparison Tool.

FIG. 4 shows the phylogenetic tree of OMP-1X proteins of *A. platys*, *A. phagocytophilum*, *A. marginate*, *E. canis*, *E. chaffeensis*, *E. ewingii*, *E. ruminantium*. The tree was constructed using DNASTAR MegAlign Clustal W method.

FIG. 5 shows the Tr1 sequence alignment of *A. platys*, *A. phagocytophilum*, and *A. marginate*. Sequences: Majority equals SEQ ID NO:133; *A. platys* seq equals SEQ ID NO:134; APH1218 equals SEQ ID NO:135; *A. marginale* equals SEQ ID NO:136.

FIG. 6A shows the phylogram of Tr1 proteins of *A. platys*, *A. phagocytophilum*, and *A. marginate*. The tree was constructed using DNASTAR MegAlign Clustal W method.

FIG. 6B shows the amino acid sequences identity between *A. platys* Tr1 and *A. phagocytophilum* Tr1 (YP_505749) or *A. marginate* AM1138 (YP_154239) were 86.4% and 73.1%, respectively.

FIG. 7 shows the OMP-1X sequence alignment of *A. platys*, *A. phagocytophilum*, and *A. marginate*. Sequences: Majority equals SEQ ID NO:137; *A. platys* equals SEQ ID NO:1; APH1219 equals SEQ ID NO:138; *A. marginale* equals SEQ ID NO:139.

FIG. 8A shows the phylogram of OMP-1X proteins of *A. platys*, *A. phagocytophilum*, and *A. marginate*. The tree was constructed using DNASTAR MegAlign Clustal W method. FIG. 8B shows the amino acid sequence identities between *A. platys* OMP-1X and *A. phagocytophilum* OMP-1X (YP_505750) or *A. marginate* outer membrane protein 1 (YP_154240) were 42.3% and 39.5%, respectively.

FIG. 9 shows the P44 sequence alignment of *A. platys*, *A. phagocytophilum*, and *A. marginate*. Sequences: Majority equals SEQ ID NO:140; *A. marginale* equals SEQ ID NO:141; *A. phagocytophilum* equals SEQ ID NO:142; *A. platys* equals SEQ ID NO:143.

FIG. 10A shows the phylogram of P44 proteins of *A. platys*, *A. phagocytophilum*, and *A. marginate*. The tree was constructed using DNASTAR MegAlign Clustal W method. FIG. 10B shows the amino acid sequences identity between *A. platys* P44ES and *A. phagocytophilum* P44-18ES (YP_505752) or *A. marginate* msp2 (YP_154245) were 55.0~56.9% and 41.5~42.1%, respectively.

FIGS. 11 and 12 show P44ES/Msp2 proteins of *A. platys*, *A. phagocytophilum*, and *A. marginate*. A total of 24 P44/Msp2s were segregated into 3 clusters. The tree was constructed using the Neighbor-Joining (NEIGHBOR program from PHYLIP) method based on the alignment generated with Clustal V; 1,000 bootstrap replications were performed. The nodes supported by bootstrap values greater than 60% are labeled.

FIGS. 13A and 13B show the sequence alignment was completed using a DNASTAR SeqMan program. Alignment of *A. platys* (*A. pl*) OMP-1X protein (FIG. 13A) and P44DS protein (FIG. 13B) with related proteins from *A. phagocytophilum* (*A. ph*), *A. marginate* (*A. ma*), *E. canis* (*E. ca*), *E. chaffeensis* (*E. ch*), *E. ewingii* (*E. ew*), and *E. ruminantium* (*E. ru*) using the Clustal W method revealed a unique region in *A. platys* (AVQEKKPPEA (SEQ ID NO: 98), box lined by dashed bar). The antigenic index and surface probability profile suggest that this region is both antigenic and surface-exposed. Sequences: *A. platys* omp-1x aa equals SEQ ID NO:144; YP-507903 equals SEQ ID NO:145; YP-505750 equals SEQ ID NO:146; YP-303524 equals SEQ ID NO:147; YP-180721 equals SEQ ID NO:148; YP154240 equals SEQ ID NO:149; AB036240 equals SEQ ID NO:150; *A. pl* (GQ868750) equals SEQ ID NO:151; *A. ph*

(YP505750) equals SEQ ID NO:152; *A. ma* (YP154240) equals SEQ ID NO:153; *E. ca* (AAK28680); *E. ch* (YP507903) equals SEQ ID NO:155; *E. ew* (AB036240) equals SEQ ID NO:156; *E. ru* (YP180721) equals SEQ ID NO:157.

FIG. 14 shows the ELISA analysis of samples from *A. platys* PCR-positive dogs (No. 1-3), *A. platys* PCR-negative dogs (No. 4-6), and *A. phagocytophilum* seropositive horse serum samples (No. 7-9) with the *A. platys* specific peptide. The y axis shows the OD₄₁₅-OD₄₉₂ values. A reaction was considered positive when the plasmas from infected dogs yielded an OD₄₁₅-OD₄₉₂ value greater than the mean OD₄₁₅-OD₄₉₂ value for negative control plasma plus 3 standard deviations (dashed line). Representative data from triplicate assays are shown.

FIG. 15 shows the alignment of *A. platys*, *A. phagocytophilum*, and *A. marginate* p44/msp2 DNA. *A. platys*-species specific primers useful for species-specific PCR diagnosis are underlined in bold. Sequences: *A. marginale* equals SEQ ID NO:158; *A. phagocytophilum* equals SEQ ID NO:159; *A. platys* equals SEQ ID NO:160; Majority equals SEQ ID NO:161.

FIG. 16 shows the *A. platys*, *A. phagocytophilum*, and *A. marginate* amino acid sequence alignment. Sequences: Majority equals SEQ ID NO:162; HV1-14 N Primer sequence removed aa (GU357494) equals SEQ ID NO:163; HV2-6 N Primer sequence removed aa (GU357495) equals SEQ ID NO:164; HV2-16 N Primer sequence removed aa (GU357496) equals SEQ ID NO:165; HV2-36 N Primer sequence removed aa (GU357497) equals SEQ ID NO:166; TW Jury (dog 431) HQ735871 equals SEQ ID NO:167; *A. platys* P44 ES 1-3 equals SEQ ID NO:168; *A. platys* P44 ES 1-4 (GU357491) equals SEQ ID NO:22; *A. platys* P44 ES 2-2 (GU357492) equals SEQ ID NO:23; *A. platys* P44 ES 3-1 (GU357493) equals SEQ ID NO:24; *A. marginale* (YP_154245) equals SEQ ID NO:141; AF200925 equals SEQ ID NO:169; AF200927 equals SEQ ID NO:170; AF290590 equals SEQ ID NO:171; AF290591 equals SEQ ID NO:172; AF290597 equals SEQ ID NO:173; AF290598 equals SEQ ID NO:174; AF290599 equals SEQ ID NO:175; *A. phagocytophilum* equals SEQ ID NO:176; P44-14 equals SEQ ID NO:177; P44-2 equals SEQ ID NO:178; P44-32 equals SEQ ID NO:179; P44-7 equals SEQ ID NO:180; P44-12 (AY164491) equals SEQ ID NO:181; P44-20 (AY164492) equals SEQ ID NO:182; P44-21 (AY164490) equals SEQ ID NO:183; P44-33 (AY164494) equals SEQ ID NO:184; P44-63 (AY164493) equals SEQ ID NO:185; *A. ph. MSP2* (YP505578) equals SEQ ID NO:186; *A. ph. MSP2* (YP505833) equals SEQ ID NO:187.

FIG. 17 shows the complete sequence assembly for the *A. platys* expression locus.

FIG. 18 shows the *A. platys* P44 alignment (DNA and protein). Sequences: Majority equals SEQ ID NO:188; H/1-14 (GU357494) equals SEQ ID NO:34; H/2-6 (GU357495) equals SEQ ID NO:35; H/2-16 (GU357496) equals SEQ ID NO:36; H/2-36 (GU357497) equals SEQ ID NO:37; TW431 HV (HQ735871) equals SEQ ID NO:189; Dog 1-3 (HQ868750) equals SEQ ID NO:190; Dog 1-4 (GU357491) equals SEQ ID NO:191; Dog 2-2 (GU357492) equals SEQ ID NO:192; Dog 3-1 (GU357493) equals SEQ ID NO:193; Majority equal SEQ ID NO:194.

FIG. 19 shows the *A. platys*-specific P44 sequence, distinct from *A. phagocytophilum* and *A. marginate* or IDEXX P44 partial sequences useful for species-specific serodiagnosis. Sequences: Majority equals SEQ ID NO:200; *A. platys* P44 from IDEXX-1 equals SEQ ID NO:201; *A. platys* P44 from IDEXX-2 equals SEQ ID NO:202; *A. platys* P44

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from IDEXX-3 equals SEQ ID NO:203; TW dog 431 P44 partial final equals SEQ ID NO:204; *A. platys* P44 ES 1-3 (GQ8687580) equals SEQ ID NO:168; *A. platys* P44 ES 1-4 (GU357491) equals SEQ ID NO:22; *A. platys* P44 ES 2-2 (GU357492) equals SEQ ID NO:23; *A. platys* P44 ES 3-1 (GU357493) equals SEQ ID NO:24; *A. phagocytophilum* P44 ES (YP505662) equals SEQ ID NO:205; *A. phagocytophilum* P44-14 (YP505746.1) equals SEQ ID NO:206; P44-2 (YP505715.1) equals SEQ ID NO:178; P44-32 (YP505802.1) equals SEQ ID NO:179; P44-7 (YP505662.1) equals SEQ ID NO:180; P44-12 (AY164491) equals SEQ ID NO:181; P44-20 (AY164492) equals SEQ ID NO:182; P44-21 (AY164490) equals SEQ ID NO:183; P44-33 (AY164494) equals SEQ ID NO:184; P44-63 (AY164493) equals SEQ ID NO:185.

FIG. 20 shows the comparison of the *A. platys*-specific P44 sequence to the sequences of *A. phagocytophilum* and *A. marginate*. Sequences: Majority equals SEQ ID NO:207; *A. marginate* equals SEQ ID NO:208; *A. phagocytophilum* equals SEQ ID NO:209; *A. platys* equals SEQ ID NO:30.

FIG. 21 shows the *A. platys*-specific primer regions and sequences from dog 2. Sequences: GQ868750 equals SEQ ID NO:210.

FIG. 22 shows the sequence alignment was completed using a DNASTAR SeqMan program. Alignment of *A. platys* (*A. pl*) OMP-1X protein with related proteins from *A. phagocytophilum* (*A. ph*), *A. marginate* (*A. ma*), *E. canis* (*E. ca*), *E. chaffeensis* (*E. ch*), *E. ewingii* (*E. ew*), and *E. ruminantium* (*E. ru*) using the Clustal W method revealed a unique region in *A. platys* (AVQEKKPPEA (SEQ ID NO: 98). The antigenic index and surface probability profile suggest that this region is both antigenic and surface-exposed, and distinct from those of other species. FIG. 22 also shows the identification of two regions in *A. platys* that are both antigenic and surface-exposed, and distinct from those of other species. These two regions are identified in boxes as "1" and "2". Sequences: Majority equals SEQ ID NO:211; APH1219 omp-1X aa seq equals SEQ ID NO:138; *A. marginate* omp-1X aa seq equals SEQ ID NO:139; *A. platys* dog 2 (HQ868750) equals SEQ ID NO:1; *A. platys* dog 3 (GU357491) equals SEQ ID NO:10; *A. platys* TW dog (HQ738571) equals SEQ ID NO:212.

FIG. 23 shows the sequence alignment was completed using a DNASTAR SeqMan program. Alignment of *A. platys* (*A. pl*) p44ES protein with related proteins from *A. phagocytophilum* (*A. ph*), *A. marginate* (*A. ma*), *E. canis* (*E. ca*), *E. chaffeensis* (*E. ch*), *E. ewingii* (*E. ew*), and *E. ruminantium* (*E. ru*) using the Clustal W method revealed regions in *A. platys* wherein the antigenic index and surface probability profile suggest that these regions are both antigenic and surface-exposed, and distinct from other species. These regions are identified in boxes as "1" through "6" as well as in brackets under the antigenic index and surface probability profile. Sequences: HV1-14 N Primer sequence removed aa equals SEQ ID NO:163; HV2-6 N Primer sequence removed aa equals SEQ ID NO:164; HV2-16 N Primer sequence removed aa equals SEQ ID NO:165; HV2-36 N Primer sequence removed aa equals SEQ ID NO:166; TW Jury (dog 431) (HQ735871) equals SEQ ID NO:167; *A. platys* P44 ES 1-3 equals SEQ ID NO:168; *A. platys* P44 ES 1-4 equals SEQ ID NO:22; *A. platys* P44 ES 2-2 equals SEQ ID NO:23; *A. platys* P44 ES 3-1 equals SEQ ID NO:24; *A. marginale* ORF 1021 equals SEQ ID NO:141; AF200925 equals SEQ ID NO:169; AF200927 equals SEQ ID NO:170; AF290590 equals SEQ ID NO:171; AF290591 equals SEQ ID NO:172; AF290597 equals SEQ ID NO:173; AF290598 equals SEQ ID NO:174; AF290599 equals SEQ ID NO:175;

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A. phagocytophilum equals SEQ ID NO:205; P44-14 equals SEQ ID NO:206; P44-2 equals SEQ ID NO:178; P44-32 equals SEQ ID NO:179; P44-12 (AY164491) equals SEQ ID NO:181; P44-20 (AY164492) equals SEQ ID NO:182; P44-21 (AY164490) equals SEQ ID NO:183; P44-33 (AY164494) equals SEQ ID NO:184; P44-63 (AY164493) equals SEQ ID NO:185; A ph msp 2 (YP505578) equals SEQ ID NO:186; A ph msp 2 (YP505833) equals SEQ ID NO:187.

DETAILED DESCRIPTION

Described herein are improved diagnostic tools for veterinary and human use which can be used for serodiagnosing *A. platys* in mammals, particularly in members of the Canidae family and in humans. The diagnostic tools are a group of outer membrane proteins of *A. platys* and variants thereof, referred to hereinafter as the "OMP proteins", a group of outer membrane proteins of *A. platys* and variants thereof referred to hereinafter as the "P44 proteins", and antibodies to the OMP proteins and the P44 proteins.

The present invention can be understood more readily by reference to the following detailed description of the invention and the Examples included therein.

All patents, patent applications, and publications cited herein, whether supra or infra, are hereby incorporated by reference in their entireties into this application in order to more fully describe the state of the art as known to those skilled therein as of the date of the invention described and claimed herein.

Unless otherwise expressly stated, it is in no way intended that any method or aspect set forth herein be construed as requiring that its steps be performed in a specific order. Accordingly, where a method claim does not specifically state in the claims or descriptions that the steps are to be limited to a specific order, it is in no way intended that an order be inferred, in any respect. This holds for any possible non-express basis for interpretation, including matters of logic with respect to arrangement of steps or operational flow, plain meaning derived from grammatical organization or punctuation, or the number or type of aspects described in the specification.

Definitions

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. The terminology used in the description of the embodiments herein is for describing particular embodiments only and is not intended to be limiting of the embodiments disclosed. As used in the description, the singular forms "a," "an," and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

Unless otherwise indicated, all numbers expressing quantities of ingredients, reaction conditions, and so forth used in this disclosure are to be understood as being modified in all instances by the term "about." Accordingly, unless indicated to the contrary, the numerical parameters set forth in this disclosure are approximations that may vary depending upon the desired properties sought to be obtained by the present disclosure. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of any claims, each numerical parameter should be

construed in light of the number of significant digits and ordinary rounding approaches.

Ranges can be expressed herein as from "about" one particular value, and/or to "about" another particular value. When such a range is expressed, another embodiment includes from the one particular value and/or to the other particular value. Similarly, when values are expressed as approximations, by use of the antecedent "about," it will be understood that the particular value forms another embodiment. It will be further understood that the endpoints of each of the ranges are significant both in relation to the other endpoint, and independently of the other endpoint. It is also understood that there are a number of values described herein, and that each value is also herein disclosed as "about" that particular value in addition to the value itself. For example, if the value "10" is disclosed, then "about 10" is also disclosed. It is also understood that when a value is disclosed that "less than or equal to" the value, "greater than or equal to the value" and possible ranges between values are also disclosed, as appropriately understood by the skilled artisan. For example, if the value "10" is disclosed the "less than or equal to 10" as well as "greater than or equal to 10" is also disclosed. It is also understood that throughout the application, data are provided in a number of different formats, and that these data, represent endpoints, starting points, and ranges for any combination of the data points. For example, if a particular data point "10" and a particular data point 15 are disclosed, it is understood that greater than, greater than or equal to, less than, less than or equal to, and equal to 10 and 15 are considered disclosed as well as between 10 and 15. It is also understood that each unit between two particular units is also disclosed. For example, if 10 and 15 are disclosed, then 11, 12, 13, and 14 are also disclosed.

The term "subject" means an individual. In one aspect, a subject is a mammal such as a primate, and, more preferably, a human. Non-human primates include marmosets, monkeys, chimpanzees, gorillas, orangutans, and gibbons, to name a few. The term "subject" also includes domesticated animals, such as cats, dogs, etc., livestock (for example, cattle (cows), horses, pigs, sheep, goats, etc.), laboratory animals (for example, ferret, chinchilla, mouse, rabbit, rat, gerbil, guinea pig, etc.) and avian species (for example, chickens, turkeys, ducks, pheasants, pigeons, doves, parrots, cockatoos, geese, etc.). Subjects can also include, but are not limited to fish (for example, zebrafish, goldfish, tilapia, salmon, and trout), amphibians and reptiles. As used herein, a "subject" is the same as a "patient," and the terms can be used interchangeably.

As used herein, the term "amino acid sequence" refers to a list of abbreviations, letters, characters or words representing amino acid residues. The amino acid abbreviations used herein are conventional one letter codes for the amino acids and are expressed as follows: A, alanine; C, cysteine; D aspartic acid; E, glutamic acid; F, phenylalanine; G, glycine; H histidine; I isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; Y, tyrosine.

"Polypeptide" as used herein refers to any peptide, oligopeptide, polypeptide, gene product, expression product, or protein. A polypeptide is comprised of consecutive amino acids. The term "polypeptide" encompasses naturally occurring or synthetic molecules. The terms "polypeptide," "peptide," and "protein" can be used interchangeably.

In addition, as used herein, the term "polypeptide" refers to amino acids joined to each other by peptide bonds or

modified peptide bonds, e.g., peptide isosteres, etc. and may contain modified amino acids other than the 20 gene-encoded amino acids. The polypeptides can be modified by either natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. The same type of modification can be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide can have many types of modifications. Modifications include, without limitation, acetylation, acylation, ADP-ribosylation, amidation, covalent cross-linking or cyclization, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, disulfide bond formation, demethylation, formation of cysteine or pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pergylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, and transfer-RNA mediated addition of amino acids to protein such as arginylation. (See *Proteins—Structure and Molecular Properties* 2nd Ed., T. E. Creighton, W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983)).

As used herein, "isolated polypeptide" or "purified polypeptide" is meant to mean a polypeptide (or a fragment thereof) that is substantially free from the materials with which the polypeptide is normally associated in nature. The polypeptides of the invention, or fragments thereof, can be obtained, for example, by extraction from a natural source (for example, a mammalian cell), by expression of a recombinant nucleic acid encoding the polypeptide (for example, in a cell or in a cell-free translation system), or by chemically synthesizing the polypeptide. In addition, polypeptide fragments may be obtained by any of these methods, or by cleaving full length proteins and/or polypeptides.

As used herein, "peptidomimetic" means a mimetic of a function of a protein which includes some alteration of the normal peptide chemistry. Peptidomimetics typically are short sequences of amino acids that in biological properties, mimic the function(s) of a particular protein. Peptide analogs enhance some property of the original peptide, such as increase stability, increased efficacy, enhanced delivery, increased half life, etc. Methods of making peptidomimetics based upon a known polypeptide sequence is described, for example, in U.S. Pat. Nos. 5,631,280; 5,612,895; and 5,579,250. Use of peptidomimetics can involve the incorporation of a non-amino acid residue with non-amide linkages at a given position. One embodiment of the present invention is a peptidomimetic wherein the compound has a bond, a peptide backbone or an amino acid component replaced with a suitable mimic. Some non-limiting examples of unnatural L- or D-amino acids which may be suitable amino acid mimics include β -alanine, L- α -amino butyric acid, L- γ -amino butyric acid, L- α -amino isobutyric acid, L- ϵ -amino caproic acid, 7-amino heptanoic acid, L-aspartic acid, L-glutamic acid, N- ϵ -Boc-N- α -CBZ-L-lysine, N- ϵ -Boc-N- α -Fmoc-L-lysine, L-methionine sulfone, L-norleucine, L-norvaline, N- α -Boc-N- δ -CBZ-L-ornithine, N- δ -Boc-N- α -CBZ-L-ornithine, Boc-p-nitro-L-phenylalanine, Boc-hydroxyproline, and Boc-L-thioproline.

The word “or” as used herein means any one member of a particular list and also includes any combination of members of that list.

The phrase “nucleic acid” as used herein refers to a naturally occurring or synthetic oligonucleotide or polynucleotide, whether DNA or RNA or DNA-RNA hybrid, single-stranded or double-stranded, sense or antisense, which is capable of hybridization to a complementary nucleic acid by Watson-Crick base-pairing. Nucleic acids of the invention can also include nucleotide analogs (e.g., BrdU), and non-phosphodiester internucleoside linkages (e.g., peptide nucleic acid (PNA) or thiodiester linkages). In particular, nucleic acids can include, without limitation, DNA, RNA, cDNA, gDNA, ssDNA, dsDNA or any combination thereof.

As used herein, “isolated nucleic acid” or “purified nucleic acid” is meant to mean DNA that is free of the genes that, in the naturally-occurring genome of the organism from which the DNA of the invention is derived, flank the gene. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, such as an autonomously replicating plasmid or virus; or incorporated into the genomic DNA of a prokaryote or eukaryote (e.g., a transgene); or which exists as a separate molecule (for example, a cDNA or a genomic or cDNA fragment produced by PCR, restriction endonuclease digestion, or chemical or in vitro synthesis). It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence. The term “isolated nucleic acid” also refers to RNA, e.g., an mRNA molecule that is encoded by an isolated DNA molecule, or that is chemically synthesized, or that is separated or substantially free from at least some cellular components, for example, other types of RNA molecules or polypeptide molecules.

As used herein, “sample” is meant to mean an animal; a tissue or organ from an animal; a cell (either within a subject, taken directly from a subject, or a cell maintained in culture or from a cultured cell line); a cell lysate (or lysate fraction) or cell extract; or a solution containing one or more molecules derived from a cell or cellular material (e.g. a polypeptide or nucleic acid), which is assayed as described herein. A sample may also be any body fluid or excretion (for example, but not limited to, blood, urine, stool, saliva, tears, bile) that contains cells or cell components.

As used herein, “modulate” is meant to mean to alter, by increasing or decreasing.

As used herein, “effective amount” of a compound is meant to mean a sufficient amount of the compound to provide the desired effect. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of disease (or underlying genetic defect) that is being treated, the particular compound used, its mode of administration, and the like. Thus, it is not possible to specify an exact “effective amount.” However, an appropriate “effective amount” may be determined by one of ordinary skill in the art using only routine experimentation.

As used herein, “prevent” is meant to mean minimize the chance that a subject who has an increased susceptibility for developing *A. platys* infection will develop *A. platys* infection.

As used herein, “specifically binds” is meant that an antibody recognizes and physically interacts with its cognate antigen (for example, the disclosed *A. platys* peptides) and does not significantly recognize and interact with other antigens; such an antibody may be a polyclonal antibody or

a monoclonal antibody, which are generated by techniques that are well known in the art.

As used herein, “probe,” “primer,” or oligonucleotide is meant to mean a single-stranded DNA or RNA molecule of defined sequence that can base-pair to a second DNA or RNA molecule that contains a complementary sequence (the “target”). The stability of the resulting hybrid depends upon the extent of the base-pairing that occurs. The extent of base-pairing is affected by parameters such as the degree of complementarity between the probe and target molecules and the degree of stringency of the hybridization conditions. The degree of hybridization stringency is affected by parameters such as temperature, salt concentration, and the concentration of organic molecules such as formamide, and is determined by methods known to one skilled in the art. Probes or primers specific for nucleic acids capable of encoding the disclosed *A. platys* peptides (for example, genes and/or mRNAs) have at least 80%-90% sequence complementarity, preferably at least 91%-95% sequence complementarity, more preferably at least 96%-99% sequence complementarity, and most preferably 100% sequence complementarity to the region of the nucleic acid capable of encoding the disclosed *A. platys* peptides to which they hybridize. Probes, primers, and oligonucleotides may be detectably-labeled, either radioactively, or non-radioactively, by methods well-known to those skilled in the art. Probes, primers, and oligonucleotides are used for methods involving nucleic acid hybridization, such as: nucleic acid sequencing, reverse transcription and/or nucleic acid amplification by the polymerase chain reaction, single stranded conformational polymorphism (SSCP) analysis, restriction fragment polymorphism (RFLP) analysis, Southern hybridization, Northern hybridization, in situ hybridization, and electrophoretic mobility shift assay (EMSA).

As used herein, “specifically hybridizes” is meant to mean that a probe, primer, or oligonucleotide recognizes and physically interacts (that is, base-pairs) with a substantially complementary nucleic acid (for example, a nucleic acid capable of encoding the disclosed *A. platys* peptides) under high stringency conditions, and does not substantially base pair with other nucleic acids.

As used herein, “high stringency conditions” is meant to mean conditions that allow hybridization comparable with that resulting from the use of a DNA probe of at least 40 nucleotides in length, in a buffer containing 0.5 M NaHPO₄, pH 7.2, 7% SDS, 1 mM EDTA, and 1% BSA (Fraction V), at a temperature of 65° C., or a buffer containing 48% formamide, 4.8×SSC, 0.2 M Tris-Cl, pH 7.6, 1×Denhardt’s solution, 10% dextran sulfate, and 0.1% SDS, at a temperature of 42° C. Other conditions for high stringency hybridization, such as for PCR, Northern, Southern, or in situ hybridization, DNA sequencing, etc., are well-known by those skilled in the art of molecular biology. (See, for example, F. Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y., 1998).

Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the disclosure are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently contains certain errors necessarily resulting from the standard deviation found in their respective testing measurements. Every numerical range given throughout this specification will include every narrower numerical range that falls within such broader numerical range, as if such narrower numerical ranges were all expressly written herein.

In addition, where features or aspects of the inventions are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Compositions

Described herein are the components to be used to prepare the disclosed compositions as well as the compositions themselves to be used within the methods disclosed herein. These and other materials are disclosed herein, and it is understood that when combinations, subsets, interactions, groups, etc. of these materials are disclosed that while specific reference of each various individual and collective combinations and permutation of these compounds may not be explicitly disclosed, each is specifically contemplated and described herein. Thus, if a class of molecules A, B, and C are disclosed as well as a class of molecules D, E, and F and an example of a combination molecule, A-D is disclosed, then even if each is not individually recited each is individually and collectively contemplated meaning combinations, A-E, A-F, B-D, B-E, B-F, C-D, C-E, and C-F are considered disclosed. Likewise, any subset or combination of these is also disclosed. Thus, for example, the sub-group of A-E, B-F, and C-E would be considered disclosed. This concept applies to all aspects of this application including, but not limited to, steps in methods of making and using the disclosed compositions. Thus, if there are a variety of additional steps that can be performed it is understood that each of these additional steps can be performed with any specific embodiment or combination of embodiments of the disclosed methods.

Also disclosed are the components to be used to prepare the disclosed compositions as well as the compositions themselves to be used within the methods disclosed herein. These and other materials are disclosed herein, and it is understood that when combinations, subsets, interactions, groups, etc. of these materials are disclosed that while specific reference of each various individual and collective combinations and permutation of these compounds may not be explicitly disclosed, each is specifically contemplated and described herein.

Described herein are compositions and methods for the detection of *Anaplasma platys* in a sample obtained from an animal, particularly a member of the Canidae family. One embodiment of the invention provides a PCR-based method for the amplification of minute amounts of *A. platys* DNA isolated from canines. For example, and not to be limiting, amplification of DNA can be carried out with a high fidelity Taq polymerase.

Polynucleotides

Described herein are isolated or purified nucleotides. For example, disclosed herein are *Anaplasma platys* nucleotides. The disclosed *Anaplasma platys* nucleotides can be used in one or more of the methods disclosed herein.

As used herein, "*Anaplasma platys* nucleotides" or "*Anaplasma platys* polynucleotides" refers to the P44 or the OMP-1X nucleotide sequences as well as combinations or fragments thereof described herein. For example, *Anaplasma platys* nucleotides include, but are not limited to, the P44 nucleotide sequences provided in the Figures as well as the sequences provided in SEQ ID NOs: 30-38, SEQ ID NOs: 46-51, combinations thereof as well as fragments thereof. Such sequences can also be referred to as *Anaplasma platys* P44 nucleotides or *Anaplasma platys* P44

polynucleotides. Additional examples of *Anaplasma platys* P44 nucleotides include, but are not limited to Genebank Accession Nos: GQ868750, GU357491, GU357492, GU357493, GU357494, GU357495, GU357496, GU357497, and HQ738571.

Also disclosed herein are regions of the *Anaplasma platys* P44 and OMP-1X peptides that have been identified as being highly antigenic as identified through the Jameson-Wolf method as well through a surface probability plot analysis. These regions are herein referred to as a "Box" regions. For example, six regions of the *Anaplasma platys* P44 protein sequence have been identified in FIGS. 19 and 23. These six regions, from the N-terminal to the C-terminal regions are herein referred to as "P44 Box 1", "P44 Box 2", "P44 Box 3", "P44 Box 4", "P44 Box 5", and "P44 Box 6", respectively. In addition, two regions of the *Anaplasma platys* OMP-1X protein sequence have been identified in FIG. 22. These two regions, from the N-terminal to the C-terminal regions are herein referred to as "OMP-1X Box 1" and "OMP-1X Box 2", respectively.

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "P44 Box 1". P44 Box 1 includes, but is not limited to, SEQ ID NO: 46. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the sequence of "P44 Box 1". For example, P44 Box 1 primers can include, but are not limited to: SEQ ID NOs: 52 and 53.

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "P44 Box 2". P44 Box 2 includes, but is not limited to, SEQ ID NO: 47. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the sequence of "P44 Box 2". For example, P44 Box 1 primers can include, but are not limited to: SEQ ID NOs: 54 and 55.

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "P44 Box 3". P44 Box 3 includes, but is not limited to, SEQ ID NO: 48. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the sequence of "P44 Box 3". For example, P44 Box 1 primers can include, but are not limited to: SEQ ID NOs: 56 and 57.

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "P44 Box 4". P44 Box 4 includes, but is not limited to, SEQ ID NO: 49. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the sequence of "P44 Box 4". For example, P44 Box 1 primers can include, but are not limited to: SEQ ID NOs: 58 and 59.

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "P44 Box 5". P44 Box 5 includes, but is not limited to, SEQ ID NO: 50. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the sequence of "P44 Box 5". For example, P44 Box 1 primers can include, but are not limited to: SEQ ID NOs: 60 and 61.

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "P44 Box 6". P44 Box 6 includes, but is not limited to, SEQ ID NO: 51. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the

sequence of "P44 Box 6". For example, P44 Box 1 primers can include, but are not limited to: SEQ ID NOs: 62 and 63.

Also disclosed are primers that can be used to amplify one or more *Anaplasma platys* P44 nucleotides. Examples include, but are not limited to SEQ ID NOs: 82-91.

Anaplasma platys nucleotides include, but are not limited to, the OMP-1X nucleotide sequences provided in the Figures as well as the sequences provided in SEQ ID NOs: 11-17, combinations thereof as well as fragments thereof. Such sequences can also be referred to as *Anaplasma platys* OMP-1X nucleotides or *Anaplasma platys* OMP-1X polynucleotides. Other examples of *Anaplasma platys* OMP-1X nucleotides include, but are not limited to the sequences provided in GenBank Accession Nos: GQ868750, HQ738571, GU357491.

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "OMP-1X Box 1". OMP-1X Box 1 includes, but is not limited to, SEQ ID NO: 14. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the sequence of "OMP-1X Box 1".

Disclosed herein are isolated or purified polynucleotides that consist of or comprise the nucleotide sequence of "OMP-1X Box 2". OMP-1X Box 2 includes, but is not limited to, SEQ ID NO: 15. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of hybridizing to or amplifying the sequence of "OMP-1X Box 2".

The polynucleotides described herein can contain less than an entire microbial genome and can be RNA, DNA, or combinations thereof. Polynucleotides described herein can be isolated. An isolated polynucleotide is a naturally-occurring polynucleotide that is not immediately contiguous with one or both of the 5' and 3' flanking genomic sequences that it is naturally associated with. Isolated polynucleotides can also include non-naturally occurring nucleic acid molecules. In some aspects, polynucleotides can also comprise fragments that encode immunogenic polypeptides.

In some aspects, polynucleotides described herein can be probes or primers, for example, PCR primers, to detect the presence of *A. platys* polynucleotides in a biological sample. Probes are molecules capable of interacting with a target nucleic acid, typically in a sequence specific manner, for example, through hybridization. Primers are a subset of probes that can support an enzymatic manipulation and that can hybridize with a target nucleic acid sequence. A primer can be made from any combination of nucleotides or nucleotide derivatives or analogs available in the art that do not interfere with the manipulation of peptides, enzymes, or proteins. In one aspect, the primers disclosed herein can comprise any of the isolated polynucleotides described herein. For example, and not to be limiting, the isolated polynucleotide can be SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, or SEQ ID NO: 99.

The hybridization of nucleic acids is well understood in the art and hence need not be discussed herein. Typically a primer can be made from any combination of nucleotides, nucleotide derivatives, and analogs available in the art. The ability of such probes and primers to specifically hybridize

to *A. platys* polynucleotide sequences can enable the primer to be used for the detection of the presence of complementary sequences. In some embodiments, polynucleotide primers and probes of the invention described herein can hybridize to complementary sequences in a sample, including saliva, blood, plasma, serum, cerebrospinal fluid, and tissue. In some embodiments, the polynucleotides from the sample can be subjected to gel electrophoresis, size separation techniques, immobilization without size separation, and labeling. Suitable labels and methods for labeling primers are known in the art and include radioactive labels, biotin labels, fluorescent labels, bioluminescent labels, and enzyme labels.

When referring to a nucleotide sequence "N" represents any of the four common nucleotides (e.g., A, C, G, or T), "M" represents either an A or C nucleotide, "S" will be defined to mean C or G, and "Y" will be defined henceforth as C or T. For example, SEQ ID NO: 85 (GCAACCTAACACCCMAAYTCMCCACC) includes an "M" at positions 15 and 22. As such, position 15 or 22 of SEQ ID NO: 85 can be an A or C nucleotide. In addition, SEQ ID NO: 85 includes a "Y" at position 19. As such, position 9 of SEQ ID NO: 85 can be a C or T.

Primers

Disclosed herein are P44 primer sets comprising F1 through F3 and R1 through R5. Each p44 primer set comprises a first primer, i.e., forward, and a second primer, i.e., reverse, both of which can be about 10 to about 35 nucleotides in length or a primer of alternant length (e.g., 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 15-35, 20-25, 20-30, 20-35, 25-30, 25-35, 30-35). The first primer comprises a sequence that is complementary to a consecutive sequence of at least 10 nucleotides in length, within the following sequences: ATTATGTATGATTATCCTAAGTTATCTGAG (SEQ ID NO: 82), GGGATATCGGCGTTGATAGGG (SEQ ID NO: 83), and GGTTTGTGTTGCTGGTGATTGGAGG (SEQ ID NO: 84). The second primer comprises a sequence which is complementary to the inverse complement of a consecutive sequence of at least 10 nucleotides in length, within the following sequences: GCAACCTAACACCCMAAYTCMCCACC (SEQ ID NO: 85), TATACTAAAAAAGAATTAAGTCAAGAG (SEQ ID NO: 86), ATGGTAGAAAASCCCCAGCAAA (SEQ ID NO: 87), CACGTNTTTAGTTACTGCCA (SEQ ID NO: 88), and GTACTAGTCAGCGCCACTAACATCAA (SEQ ID NO: 89). As used herein, "N" represents any of the four common nucleotides (e.g., A, C, G, or T), "M" represents either an A or C nucleotide, "S" will be defined to mean C or G, and "Y" will be defined henceforth as C or T. Such primers can be useful for detecting the presence of *A. platys* in members of the Anaplasmataceae family. HVF and HVR (Table 1) are the *A. platys*-specific primers (FIG. 16). Using the nested PCR (genus-specific primer Pair F3 and R1 during the first PCR and species-specific primer pair HVF and HVR in second PCR) sensitive and *A. platys*-specific PCR can be performed. Such primers can also useful for detecting the presence of *A. platys* DNA in samples obtained from ticks or other invertebrate carriers that feed on the vertebrate hosts.

Also disclosed herein are primers that can be used to synthesize one or more of the *A. platys* polypeptides described herein. For example, disclosed herein are primers that can be used to produce an *A. platys* polypeptide comprising a sequence that is capable of encoding a multimeric *A. platys* polypeptide wherein the intervening sequence present in the full *A. platys* P44 or OMP-1X nucleotide or peptide sequence are removed. For example, disclosed herein are primers that can be used to add a restriction site

into a nucleic acid sequence described herein through inverse PCR. The nucleotide can then be digested and self-ligated to remove a specific intervening sequence. For example, SEQ ID NO: 66 (OMP-1X box 1 and box 2 Forward primer: AACATATGAATCTTGTGAGCGCGG) can be used to introduce an NdeI site in combination with SEQ ID NO: 67 (OMP-1X box 1 and box 2 Reverse primer: GGGGATCCGGCTGGGGGAGCAGAAG) which can introduce a BamHI site.

Also disclosed are primers that can be used to remove an intervening sequence between OMP-1X Box 1 and Box 2. For example, the primer pair of SEQ ID NO: 68 can be used in combination with SEQ ID NO: 69.

Also disclosed are primers that can be used to remove an intervening sequence between P44 Box 1 and Box 2. For example, the primer pair of SEQ ID NO: 70 can be used in combination with SEQ ID NO: 71.

Also disclosed are primers that can be used to remove the intervening sequence of P44 Box 1 and Box 2. For example, the primer pair of SEQ ID NO: 72 can be used in combination with SEQ ID NO: 73.

Also disclosed are primers that can be used to remove the intervening sequence of P44 Box 3 and Box 4. For example, the primer pair of SEQ ID NO: 74 can be used in combination with SEQ ID NO: 75 or SEQ ID NO: 76 can be used in combination with SEQ ID NO: 77.

Also disclosed are primers that can be used to remove the intervening sequence of P44 Box 5 and Box 6. For example, the primer pair of SEQ ID NO: 78 can be used in combination with SEQ ID NO: 79 or SEQ ID NO: 80 can be used in combination with SEQ ID NO: 81.

Also disclosed are methods for detecting *A. platys* provides a p44 primer set comprising a first primer sequence which can be complementary to a sequence of the *A. platys* p44 gene sense strand and a second primer which can be complementary to the sequence of the *A. platys* p44 gene antisense strand, amplifying the DNA in the sample using a polymerase chain reaction (PCR) and the p44 primer set, and determining the length which corresponds to the sequence or length of that portion to which the first p44 primer and the second p44 primer bind is indicative of the presence of *A. platys* in the DNA sample.

Also disclosed herein are aspects related to primers in the p44 primer set. The first p44 and the second p44 primers can be from about 10 to about 35 nucleotides in length or a primer of alternant length (e.g., 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 15-35, 20-25, 20-30, 20-35, 25-30, 25-35, 30-35). The first p44 primer, comprises a sequence which is substantially identical to the complement of a consecutive sequence of at least 10 nucleotides in length, within the following sequence: GAAGAATACGAAAGCGGCGG (SEQ ID NO: 90). In some embodiments, the primer can be capable of hybridizing to a target sequence.

The second primer comprises a sequence which can be complementary to the inverse complement of a consecutive sequence of at least 10 nucleotides in length, within the following sequence: TACTTAGGTCTTCCGCTTTCGC (SEQ ID NO: 91).

HVF and HVR (Table 1 and FIG. 16) can be useful for detecting the presence of *A. platys* in samples obtained from vertebrate animals such as humans or dogs, or from the invertebrate vectors such as brown ticks, which can transmit this pathogen from one vertebrate animal to another.

Also disclosed herein are compositions and methods for detecting the presence of *A. platys* in samples obtained from a vertebrate or invertebrate animal. The method comprises amplifying the DNA contained within the sample using a

primer set comprising primers which comprise sequences that can be complementary to select regions of the p44 gene of *A. platys* and a polymerase chain reaction (PCR) to provide a pool of PCR products, and then assaying the pool for the presence or absence of a PCR product whose length or sequence indicates that PCR product corresponds to the region of the p44 gene that is flanked by the nucleotide sequences which are complementary to the first and second members of the p44 primer set. The tools are the members of the p44 primer sets. Multiple *A. platys* p44 gene sequences are set forth in GenBank under accession No. GQ868750 and GU357491, respectively. Additional p44ES and p44 sequences were set forth in GenBank under accession No. GU357492, GU357493, GU357494, GU357495, GU357496 and GU357497.

In some embodiments, the primers in the p44 primer set can be based upon select sequences in the p44 gene of *A. platys*. The p44 gene encodes a major outer membrane protein of *A. platys*. The sequences of the first and second primers in the p44 primer set are distinct from sequences found in the closely related p44 gene homologs in *A. phagocytophilum* or *A. marginate*. The first primer in the p44 primer set can be an oligonucleotide of various lengths, including but not limited to 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 15-35, 20-25, 20-30, 20-35, 25-30, 25-35, 30-35, and 10 to 35 nucleotides in length. In some embodiments, the first primer can be at least 10 nucleotides in length. The second p44 primer in the *A. platys* primer set can be an oligonucleotide of 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 15-35, 20-25, 20-30, 20-35, 25-30, 25-35, 30-35, or 10 to 35 nucleotides in length. In one embodiment, the second p44 primer can be at least about 10 nucleotides in length. The first p44 primer can comprise a sequence which is substantially identical to the complement of consecutive sequence located between nucleotide positions 540-559 of the sense strand of the open reading frame sequence of the p44 gene of *A. platys*.

As used herein the term "substantially identical" means that the sequence is at least 90% identical, at least 95% identical, or 100% identical to a particular reference sequence (nucleotides 540-559 or 812-849) within FIG. 22.

The second p44 primer, comprises a sequence which is substantially identical to and the inverse of a consecutive sequence located between nucleotides 812-849 of the sense strand of the p44 gene of *A. platys*. The sequence of the second p44 primer is substantially identical to the complement of the inverse complement of a consecutive sequence contained within FIG. 22. In some embodiments, the primers can be capable of hybridizing to target sequences.

In specific embodiments, the first and second primers in the p44 primer set can comprise the sequences shown in Table 1. The first and second primers can also comprise sequences which are shorter by one to ten nucleotides than the sequences shown in Table 1 below. The first and second primers of the *A. platys* primer set can also comprise a sequence which is longer than the sequences shown in Table 1 below. Such sequences can have one to ten additional nucleotides attached to the 5' end of the above-listed sequences. The additional nucleotides can be selected from the group consisting of adenine, cytosine, guanine, thymine, adenylic acid, guanylic acid, and combinations thereof.

In another embodiment, the sequence of the nine first and second p44 primer sets shown in Table 1 can be based upon a comparison of the open-reading frame sequences of nine *A. platys* isolates. Such primer sets can specifically amplify the target sequence of multiple *A. platys* isolates, but not *A. phagocytophilum* or *A. marginate* isolates. The primers

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shown in Table 1 are both species-universal (e.g., F1, F2, F3, R1, R2, R3, R4, and R5) and species-specific (e.g., HVR and HVR) for *A. platys*.

Disclosed herein are isolated polynucleotides encoding an outer membrane protein of *Anaplasma platys*, or a fragment thereof. In one aspect, the outer membrane protein can be P44 or OMP-1X protein. In a further aspect, disclosed herein are isolated polynucleotides comprising any of the sequences described herein, or a fragment thereof. For example, and not to be limiting, the polynucleotide sequence can be SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, or a fragment thereof. In yet a further aspect, the isolated polynucleotide sequence can be a polynucleotide capable of encoding any peptide sequence described herein or a fragment thereof. For example and not to be limiting, the polynucleotide sequence can be a polynucleotide capable of encoding SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, or a fragment thereof. By way of further example, the polynucleotide sequences disclosed herein can also be polynucleotides capable of encoding the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19, the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, a combination or a fragment thereof. In still a further aspect, disclosed herein are isolated polynucleotides that encode the peptide sequences described herein. For example, and not to be limiting, the polynucleotide sequence can encode P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, OMP-1X Box 1, OMP-1X Box 2, OMP-1X Box 1 and

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OMP-1X Box 2, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof. By way of further example, the polynucleotide sequences disclosed herein can also be polynucleotides that can encode the amino acid sequence comprising the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof.

Also disclosed herein are isolated polynucleotides that encode variants of the proteins described herein. In one aspect, disclosed herein are isolated polynucleotides that can encode a variant of an outer membrane protein of *Anaplasma platys*, or a fragment thereof. For example, and not to be limiting, the outer membrane protein can be P44 or OMP-1X protein. In a further aspect, the polynucleotide can encode a variant that can have at least 95% identity to, for example, and not to be limiting, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19, the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, a combination or a fragment thereof. In still a further aspect, disclosed herein are isolated polynucleotides that encode the peptide sequences described herein. For example, and not to be limiting, the polynucleotide sequence can encode P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, OMP-1X Box 1, OMP-1X Box 2, OMP-1X Box 1 and

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FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof. In a further aspect, the variant can be immunoreactive with at least one antibody that binds to P44 protein, P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, OMP-1X protein, OMP-1X Box 1, OMP-1X Box 2, OMP-1X Box 1 and OMP-1X Box 2, or a fragment thereof.

Disclosed herein are polynucleotides that contain less than an entire microbial genome and can be single- or double-stranded nucleic acids. A polynucleotide can be RNA, DNA, cDNA, genomic DNA, chemically synthesized RNA or DNA or combinations thereof. The polynucleotides can be purified free of other components, such as proteins, lipids and other polynucleotides. For example, the polynucleotide can be 50%, 75%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% purified. The polynucleotides described herein can encode one or more of the polypeptides described elsewhere herein. For example, disclosed herein are polynucleotides capable of encoding the peptides described herein, for example: an *Anaplasma platys* P44 or OMP-1X protein; a variant of the *Anaplasma platys* P44 or OMP-1X protein; or an antigenic fragment of the *Anaplasma platys* P44 or OMP-1X protein, or fragments thereof. Polynucleotides can comprise other nucleotide sequences, such as sequences coding for linkers, signal sequences, TMR stop transfer sequences, transmembrane domains, or ligands useful in protein purification such as glutathione-S-transferase, histidine tag, and Staphylococcal protein A.

The polynucleotides disclosed herein can be isolated. An isolated polynucleotide is a naturally-occurring polynucleotide that is not immediately contiguous with one or both of the 5' and 3' flanking genomic sequences that it is naturally associated with. An isolated polynucleotide can be, for example, a recombinant DNA molecule of any length, provided that the nucleic acid sequences naturally found immediately flanking the recombinant DNA molecule in a naturally-occurring genome is removed or absent. Isolated polynucleotides can also include non-naturally occurring nucleic acid molecules. A nucleic acid molecule existing among hundreds to millions of other nucleic acid molecules within, for example, cDNA or genomic libraries, or gel slices containing a genomic DNA restriction digest are not to be considered an isolated polynucleotide.

The polynucleotides disclosed herein can also comprise fragments that encode immunogenic polypeptides. The polynucleotides disclosed herein can encode full-length polypeptides, polypeptide fragments, and variant or fusion polypeptides.

The polynucleotides disclosed herein can be degenerate nucleotide sequences encoding one or more of the polypeptides disclosed herein, as well as homologous nucleotide sequences that are at least about 80, 85, 90, 95, 96, 97, 98, 99% or 100% identical to the polynucleotide sequences disclosed herein and the complements thereof are also disclosed herein. Percent sequence identity can be calculated as described elsewhere herein. Degenerate nucleotide sequences are polynucleotides that encode a polypeptide of the invention or fragments thereof, but differ in nucleic acid sequence from the wild-type polynucleotide sequence, due to the degeneracy of the genetic code. Complementary DNA

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(cDNA) molecules, species homologs, and variants of *Anaplasma platys* polynucleotides that encode biologically functional *Anaplasma platys* polypeptides also are *Anaplasma platys* polynucleotides.

The polynucleotides described herein can be isolated from nucleic acid sequences present in, for example, a biological sample, such as blood, serum, saliva, or tissue from an infected individual. Polynucleotides can also be synthesized in the laboratory, for example, using an automatic synthesizer. An amplification method such as PCR can be used to amplify polynucleotides from either genomic DNA or cDNA encoding the polypeptides.

The polynucleotides disclosed herein can be used, for example, as probes or primers, for example, PCR primers, to detect the presence of *Anaplasma platys* polynucleotides in a test sample, such as a biological sample. Probes are molecules capable of interacting with a target nucleic acid, typically in a sequence specific manner, for example, through hybridization. Primers are a subset of probes that can support an enzymatic manipulation and that can hybridize with a target nucleic acid such that the enzymatic manipulation occurs. A primer can be made from any combination of nucleotides or nucleotide derivatives or analogs available in the art that do not interfere with the enzymatic manipulation.

The hybridization of nucleic acids is well understood in the art and discussed herein. Typically a probe can be made from any combination of nucleotides or nucleotide derivatives or analogs available in the art. The ability of such probes and primers to specifically hybridize to *Anaplasma platys* P44 or *Anaplasma platys* OMP-1x polynucleotide sequences will enable them to be of use in detecting the presence of complementary sequences in a given test sample. Polynucleotide probes and primers can hybridize to complementary sequences in a test sample such as a biological sample, including, but not limited to, saliva, sputum, blood, plasma, serum, urine, feces, cerebrospinal fluid, amniotic fluid, wound exudate, or tissue. Polynucleotides from the sample can be, for example, subjected to gel electrophoresis or other size separation techniques or can be immobilized without size separation. The polynucleotide probes or primers can be labeled. Suitable labels and methods for labeling probes and primers are known in the art, and include, for example, radioactive labels incorporated by nick translation or by kinase, biotin labels, fluorescent labels, chemiluminescent labels, bioluminescent labels, metal chelator labels and enzyme labels. The polynucleotides from the sample are contacted with the probes or primers under hybridization conditions of suitable stringencies.

Depending on the application, varying conditions of hybridization can be used to achieve varying degrees of selectivity of the probe or primer towards the target sequence. For applications requiring high selectivity, relatively stringent conditions can be used, such as low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50° C. to about 70° C. For applications requiring less selectivity, less stringent hybridization conditions can be used. For example, salt conditions from about 0.14 M to about 0.9M salt, at temperatures ranging from about 20° C. to about 55° C. The presence of a hybridized complex comprising the probe or primer and a complementary polynucleotide from the test sample indicates the presence of *Anaplasma platys* or an *Anaplasma platys* polynucleotide sequence in the sample.

Polypeptides

Described herein are isolated or purified polypeptides. For example, disclosed herein are isolated or purified *Anaplasma platys* polypeptides. The disclosed isolated or purified *Anaplasma platys* polypeptides can be used in one or more of the methods disclosed herein.

A polypeptide can be a polymer of three or more amino acids covalently linked by amide bonds. A polypeptide can be post-translationally modified. A purified polypeptide can be a polypeptide preparation that is substantially free of cellular material, other peptides and polypeptides, chemical precursors, synthetic chemicals, or combinations thereof.

As used herein, "*Anaplasma platys* peptides" or "*Anaplasma platys* proteins" refers to the P44 or the OMP-1X peptide sequences as well as combinations or fragments thereof described herein. For example, *Anaplasma platys* peptides include, but are not limited to, the P44 amino acid sequences provided in the Figures as well as the sequences provided in SEQ ID NOs: 21-29, SEQ ID NOs: 39-45, SEQ ID NOs: 92-98, combinations thereof as well as fragments thereof. Such sequences can also be referred to as *Anaplasma platys* P44 peptides or *Anaplasma platys* P44 proteins. Other examples of *Anaplasma platys* P44 peptides include, but are not limited to the sequences provided in GenBank Accession Nos: GQ868750, GU357491, GU357492, GU357493, HQ738571, GU357494, GU357495, GU357496, and GU357497.

Anaplasma platys peptides also include, but are not limited to, the OMP-1X amino acid sequences provided in the Figures as well as the sequences provided in SEQ ID NOs: 1-11, combinations thereof as well as fragments thereof. Such sequences can also be referred to as *Anaplasma platys* OMP-1X proteins. Other examples of *Anaplasma platys* OMP-1X peptides include, but are not limited to the sequences provided in GenBank Accession Nos: GQ868750, HQ738571, and GU357491.

Also disclosed herein are regions of the *Anaplasma platys* P44 and OMP-1X peptides that have been identified as being highly antigenic as identified through the Jameson-Wolf method as well through a surface probability plot analysis. These regions are herein referred to as a "Box" regions. For example, six regions of the *Anaplasma platys* P44 protein sequence have been identified in FIGS. 19 and 23. These six regions, from the N-terminal to the C-terminal regions are herein referred to as "P44 Box 1", "P44 Box 2", "P44 Box 3", "P44 Box 4", "P44 Box 5", and "P44 Box 6", respectively. In addition, two regions of the *Anaplasma platys* OMP-1X protein sequence have been identified in FIG. 22. These two regions, from the N-terminal to the C-terminal regions are herein referred to as "OMP-1X Box 1" and "OMP-1X Box 2", respectively.

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "P44 Box 1". P44 Box 1 includes, but is not limited to, the P44 Box 1 amino acid sequences identified in FIG. 19 or 23, for example the sequence from about position 22 to about position 39 of FIG. 19 or the sequence from about position 40 to about position 64 of FIG. 23. In addition, P44 Box 1 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 39, SEQ ID NO: 92, SEQ ID NOs: 100-103, the amino acid sequences from about position 22 to about position 39 of SEQ ID NOs: 21-24, or the amino acid sequence encoded by SEQ ID NO: 46. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "P44 Box 1".

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "P44 Box

2". P44 Box 2 includes, but is not limited to, the P44 Box 2 amino acid sequences identified in FIG. 19 or 23, for example the sequence from about position 77 to about position 85 of FIG. 19 or the sequence from about position 102 to about position 111 of FIG. 23. In addition, P44 Box 2 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NOs: 104-107, the amino acid sequences from about position 77 to about position 85 of SEQ ID NOs: 21-24, or the amino acid sequence encoded by SEQ ID NO: 47. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "P44 Box 2".

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "P44 Box 3". P44 Box 3 includes, but is not limited to, the P44 Box 3 amino acid sequences identified in FIG. 19 or 23, for example the sequence from about position 151 to about position 190 of FIG. 19 or the sequence from about position 178 to about position 222 of FIG. 23. In addition, P44 Box 3 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NOs: 108-111, the amino acid sequences from about position 151 to about position 191 of SEQ ID NOs: 21-24, or the amino acid sequence encoded by SEQ ID NO: 48. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "P44 Box 3".

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "P44 Box 4". P44 Box 4 includes, but is not limited to, the P44 Box 4 amino acid sequences identified in FIG. 19 or 23, for example the sequence from about position 227 to about position 234 of FIG. 19 or the sequence from about position 259 to about position 266 of FIG. 23. In addition, P44 Box 4 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NOs: 112-115, the amino acid sequences from about position 207 to about position 214 of SEQ ID NOs: 21-24, or the amino acid sequence encoded by SEQ ID NO: 49. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "P44 Box 4".

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "P44 Box 5". P44 Box 5 includes, but is not limited to, the P44 Box 5 amino acid sequences identified in FIG. 19 or 23, for example the sequence from about position 276 to about position 308 of FIG. 19 or the sequence from about position 319 to about position 340 of FIG. 23. In addition, P44 Box 5 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NOs: 116-119, the amino acid sequences from about position 248 to about position 269 of SEQ ID NOs: 21-24, or the amino acid sequence encoded by SEQ ID NO: 50. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "P44 Box 5".

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "P44 Box 6". P44 Box 6 includes, but is not limited to, the P44 Box 6 amino acid sequences identified in FIG. 19 or 23, for example the sequence from about position 417 to about position 426 of FIG. 19 or the sequence from about position 451 to about position 460 of FIG. 23. In addition, P44 Box 6 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 44, SEQ ID NO: 97, SEQ ID NOs: 120-123,

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the amino acid sequences from about position 378 to about position 386 of SEQ ID NOs: 21-24, or the amino acid sequence encoded by SEQ ID NO: 51. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "P44 Box 6".

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "OMP-1X Box 1". OMP-1X Box 1 includes, but is not limited to, the OMP-1X Box 1 amino acid sequences identified in FIG. 22, for example the sequence from about position 66 to about position 192 of FIG. 22. In addition, OMP-1X Box 1 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 2, SEQ ID NO: 6, or SEQ ID NO: 14. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "OMP-1X Box 1".

Disclosed herein are isolated or purified polypeptides that consist of or comprise the amino acid sequence of "OMP-1X Box 2". OMP-1X Box 2 includes, but is not limited to, the OMP-1X Box 2 amino acid sequences identified in FIG. 22, for example the sequence from about position 241 to about position 309 of FIG. 22. In addition, OMP-1X Box 2 includes, but is not limited to, the amino acid sequences of SEQ ID NO: 3, SEQ ID NO: 7, or SEQ ID NO: 15. Also disclosed herein are isolated or purified polynucleotides that consist of or comprise a polynucleotide sequence capable of encoding the amino acid sequence of "OMP-1X Box 2".

Also described herein are purified polypeptides comprising the sequences outlined in FIG. 17, or at least about 10 contiguous amino acids of the sequence from FIG. 17 wherein the at least 10 contiguous amino acids are chosen from amino acids 300-410. In some aspects, the polypeptides described herein also inherently disclose the nucleotide sequence as related to the amino acids sequence 300-410 from FIG. 17.

In one aspect, described herein are purified polypeptides comprising at least about 8, 10, 15, 20, 30, 40, 50, or more contiguous amino acids, wherein the contiguous amino acids can be chosen from amino acids 300-410 from FIG. 17.

Disclosed herein are purified polypeptides that can either be full-length polypeptides or fragments of polypeptides. For example, fragments of polypeptides disclosed herein can comprise about 8, 10, 15, 20, 30, 40, 50, or more amino acids of polypeptides of the aspects described herein. Variant polypeptides can be at least about 90, 96, 98, or 99% identical to the polypeptide sequences shown in FIGS. 17 and 22. Variant polypeptides can have one or more conservative amino acid variations or other minor modifications and retain biological activity, i.e., are biologically functional equivalents. A biologically active equivalent can have substantially equivalent function when compared to the corresponding wild-type polypeptide.

Described herein are isolated or purified polypeptides comprising a sequence chosen from the following: a *Anaplasma platys* P44 protein, a variant of an *Anaplasma platys* P44 protein, or an antigenic fragment of an *Anaplasma platys* P44 protein. In one aspect, the *Anaplasma platys* P44 protein can comprise or consist of: P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ

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ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof.

In a further aspect, the *Anaplasma platys* P44 protein can comprise or consist of a variant of: P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the

amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof.

It is understood that one way to define the variants and derivatives of the disclosed proteins herein is to define them in terms of homology/identity to specific known sequences. Specifically disclosed are variants of *A. platys* peptides and other proteins or peptides herein disclosed which have at least, 70% or at least 75% or at least 80% or at least 85% or at least 90% or at least 95% homology to the *A. platys* peptides specifically recited herein. Those of skill in the art readily understand how to determine the homology of two proteins.

As this specification discusses various polypeptides and polypeptide sequences it is understood that the nucleic acids that can encode those polypeptide sequences are also disclosed. This would include all degenerate sequences related to a specific polypeptide sequence, i.e. all nucleic acids having a sequence that encodes one particular polypeptide sequence as well as all nucleic acids, including degenerate nucleic acids, encoding the disclosed variants and derivatives of the protein sequences. Thus, while each particular nucleic acid sequence may not be written out herein, it is understood that each and every sequence is in fact disclosed and described herein through the disclosed polypeptide sequences.

In yet a further aspect, the *Anaplasma platys* P44 protein can comprise or consist of an antigenic fragment of: P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid sequence comprising the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19, the amino acid from about position 276 to about position 294 of FIG. 19, or the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19. In still a further aspect, the *Anaplasma platys* P44 proteins

described herein can comprise or consist of a combination of one or more of the sequences described herein.

In one aspect, the variants or antigenic fragments of the *Anaplasma platys* P44 proteins described herein can be immunoreactive with at least one antibody that binds to their corresponding peptide sequence.

Also described herein are isolated or purified polypeptides that can comprise a sequence that is at least 95% identical to an *Anaplasma platys* P44 protein, a variant of the *Anaplasma platys* P44 protein, or an antigenic fragment of the *Anaplasma platys* P44 protein. Thus, in one aspect, the polypeptides described herein can be at least 95% identical to: P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19, the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof.

In a further aspect, the polypeptides described herein can be at least 95% identical to a variant of: P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position

102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof.

In yet a further aspect, the polypeptides described herein can be at least 95% identical to an antigenic fragment of: P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, or the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19. In still a further aspect, the polypeptides described herein can be at least 95% identical to one or more of the peptide sequences described herein. In still a further aspect, the

Anaplasma platys P44 proteins described herein can comprise or consist of a combination of one or more of the sequences described herein.

In one aspect, the variants or antigenic fragments can be at least 95% identical to the *Anaplasma platys* P44 proteins described herein can be immunoreactive with at least one antibody that binds to their corresponding peptide sequence.

In one aspect, the isolated polypeptides described herein can be: the P44 Box 1 protein, the P44 Box 2 protein, the P44 Box 3 protein, the P44 Box 4 protein, the P44 Box 5 protein, the P44 Box 6 protein; a variant of the P44 Box 1 protein, the P44 Box 2 protein, the P44 Box 3 protein, the P44 Box 4 protein, the P44 Box 5 protein, the P44 Box 6 protein; or an antigenic fragment of the P44 Box 1 protein, the P44 Box 2 protein, the P44 Box 3 protein, the P44 Box 4 protein, the P44 Box 5 protein, the P44 Box 6 protein.

Furthermore, described herein are isolated or purified polypeptides comprising a sequence chosen from the following: a *Anaplasma platys* OMP-1X protein, a variant of the *Anaplasma platys* OMP-1X protein, or an antigenic fragment of the *Anaplasma platys* OMP-1X protein. In one aspect, the *Anaplasma platys* OMP-1X protein can comprise or consist of: OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof.

In a further aspect, the *Anaplasma platys* OMP-1X protein can comprise or consist of a variant of: OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof.

In yet a further aspect, the *Anaplasma platys* OMP-1X protein can comprise or consist of an antigenic fragment of: OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from

about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, or a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22. In still a further aspect, the *Anaplasma platys* OMP-1X proteins described herein can comprise or consist of a combination of one or more of the sequences described herein.

In one aspect, the variants or antigenic fragments of the *Anaplasma platys* OMP-1X proteins described herein can be immunoreactive with at least one antibody that binds to their corresponding peptide sequence.

Also described herein are isolated or purified polypeptides that can comprise a sequence that is at least 95% identical to an *Anaplasma platys* OMP-1X protein, a variant of the *Anaplasma platys* OMP-1X protein, or an antigenic fragment of the *Anaplasma platys* OMP-1X protein. Thus, in one aspect, the polypeptides described herein can be at least 95% identical to: OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof.

In a further aspect, the polypeptides described herein can be at least 95% identical to a variant of: OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof.

In yet a further aspect, the polypeptides described herein can be at least 95% identical to an antigenic fragment of: OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of

FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, or a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22. In still a further aspect, the *Anaplasma platys* OMP-1X proteins described herein can comprise or consist of a combination of one or more of the sequences described herein. In still a further aspect, the polypeptides described herein can be at least 95% identical to one or more of the peptide sequences described herein. In still a further aspect, the *Anaplasma platys* OMP-1X proteins described herein can comprise or consist of a combination of one or more of the sequences described herein.

In one aspect, the variants or antigenic fragments can be at least 95% identical to the *Anaplasma platys* OMP-1X proteins described herein can be immunoreactive with at least one antibody that binds to their corresponding peptide sequence.

In one aspect, the isolated polypeptides described herein can be: the OMP-1X protein, the OMP-1X Box 1 protein, or the OMP-1X Box 2 protein; a variant of the OMP-1X protein, the OMP-1X Box 1 protein, or the OMP-1X Box 2 protein; or an antigenic fragment of the OMP-1X protein, the OMP-1X Box 1 protein, or the OMP-1X Box 2 protein.

Also disclosed herein are isolated polynucleotides that encode the polypeptides described herein. A purified polypeptide can further comprising a carrier. A purified polypeptide can be in a multimeric form. A purified polypeptide can be linked to an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, a heterologous polypeptide or a combination thereof.

Purified polypeptides described herein can either be full-length polypeptides or fragments of polypeptides. For example, fragments of polypeptides described herein can comprise about 10, 15, 20, 50, 75, 100, 150, 200, 250 or more amino acids of polypeptides of the invention. For example, and not to be limiting, variant polypeptides can be at least about 80, or about 90, 96, 98, or 99% identical to the polypeptide sequences shown in SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof, and are also polypeptides of the invention. Variant polypeptides have one or more conservative amino acid variations or other minor modifications and retain biological activity, i.e., are biologically functional equivalents. A biologically active equivalent has substantially equivalent function when compared to the corresponding wild-type polypeptide.

Percent sequence identity has an art recognized meaning and there are a number of methods to measure identity between two polypeptide or polynucleotide sequences. See, e.g., Lesk, Ed., Computational Molecular Biology, Oxford University Press, New York, (1988); Smith, Ed., Biocomputing: Informatics And Genome Projects, Academic Press, New York, (1993); Griffin & Griffin, Eds., Computer Analysis Of Sequence Data, Part I, Humana Press, New Jersey,

(1994); von Heinje, Sequence Analysis In Molecular Biology, Academic Press, (1987); and Gribskov & Devereux, Eds., Sequence Analysis Primer, M Stockton Press, New York, (1991). Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux et al., Nuc. Acids Res. 12:387 (1984)), BLASTP, BLASTN, FASTA (Atschul et al., J. Molec. Biol. 215:403 (1990)), and Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711) which uses the local homology algorithm of Smith and Waterman (Adv. App. Math., 2:482-489 (1981)). For example, the computer program ALIGN which employs the FASTA algorithm can be used, with an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2.

When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, about 95% identical to a reference sequence, the parameters are set such that the percentage of identity is calculated over the full length of the reference polynucleotide or polypeptide and that gaps in identity of up to 5% of the total number of nucleotides or amino acids in the reference polynucleotide or polypeptide are allowed.

Variants can generally be identified by modifying one of the polypeptide sequences of the invention, and evaluating the properties of the modified polypeptide to determine if it is a biological equivalent. A variant is a biological equivalent if it reacts substantially the same as a polypeptide of the invention in an assay such as an immunohistochemical assay, an enzyme-linked immunosorbent Assay (ELISA), a radioimmunoassay (RIA), immunoenzyme assay or a western blot assay, e.g. has 90-110% of the activity of the original polypeptide. In one embodiment, the assay is a competition assay wherein the biologically equivalent polypeptide is capable of reducing binding of the polypeptide of the invention to a corresponding reactive antigen or antibody by about 80, 95, 99, or 100%. An antibody that specifically binds a corresponding wild-type polypeptide also specifically binds the variant polypeptide. Variant polypeptides of the invention can comprise about 1, 2, 3, 4, 5, 10, or 20 conservative amino acid substitutions.

A conservative substitution is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

The polypeptides described herein can further comprise a signal (or leader) sequence that co-translationally or post-translationally directs transfer of the protein. The polypeptide can also comprise a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide can be conjugated to an immunoglobulin Fc region or bovine serum albumin.

The polypeptides described herein can be covalently or non-covalently linked to an amino acid sequence to which the polypeptide is not normally associated with in nature, i.e., a heterologous amino acid sequence. A heterologous amino acid sequence can be from a non-*Anaplasma platys* organism (e.g., an *Anaplasma phagocytophilum* organism), a synthetic sequence, or an *Anaplasma platys* sequence not

usually located at the carboxy or amino terminus of a polypeptide of the invention. Additionally, a polypeptide can be covalently or non-covalently linked to compounds or molecules other than amino acids. For example, a polypeptide can be linked to an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, or a combination thereof. In one embodiment of the invention a protein purification ligand can be one or more C amino acid residues at, for example, the amino terminus or carboxy terminus of a polypeptide of the invention. An amino acid spacer is a sequence of amino acids that are not usually associated with a polypeptide of the invention in nature. An amino acid spacer can comprise about 1, 5, 10, 20, 100, or 1,000 amino acids.

If desired, a polypeptide can be a fusion protein, which can also contain other amino acid sequences, such as amino acid linkers, amino acid spacers, signal sequences, TMR stop transfer sequences, transmembrane domains, as well as ligands useful in protein purification, such as glutathione-S-transferase, histidine tag, and Staphylococcal protein A, or combinations thereof. More than one polypeptide of the invention can be present in a fusion protein. Fragments of polypeptides of the invention can be present in a fusion protein of the invention. A fusion protein of the invention can comprise one or more of *Anaplasma platys* polypeptides described herein, fragments thereof, or combinations thereof. A fusion protein can also comprise multiple copies of a same *Anaplasma platys* polypeptide or combination of different *Anaplasma platys* polypeptides described herein.

Polypeptides of the invention can be in a multimeric form. That is, a polypeptide can comprise one or more copies of an *Anaplasma platys* polypeptide of the invention or a combination thereof. A multimeric polypeptide can be a multiple antigen peptide (MAP). See e.g., Tam, J. Immunol. Methods, 196:17-32 (1996).

Polypeptides of the invention can comprise an antigen that is recognized by an antibody specific for *Anaplasma platys* P44 or *Anaplasma platys* OMP-1X. The antigen can comprise one or more epitopes (i.e., antigenic determinants). An epitope can be a linear epitope, sequential epitope or a conformational epitope. Epitopes within a polypeptide of the invention can be identified by several methods. See, e.g., U.S. Pat. No. 4,554,101; Jameson & Wolf, CABIOS 4:181-186 (1988). For example, a polypeptide of the invention can be isolated and screened. A series of short peptides, which together span an entire polypeptide sequence, can be prepared by proteolytic cleavage. By starting with, for example, 100-mer polypeptide fragments, each fragment can be tested for the presence of epitopes recognized in an ELISA. For example, in an ELISA assay an *Anaplasma platys* polypeptide, such as a 100-mer polypeptide fragment, is attached to a solid support, such as the wells of a plastic multi-well plate. A population of antibodies are labeled, added to the solid support and allowed to bind to the unlabeled antigen, under conditions where non-specific absorption is blocked, and any unbound antibody and other proteins are washed away. Antibody binding is detected by, for example, a reaction that converts a colorless substrate into a colored reaction product. Progressively smaller and overlapping fragments can then be tested from an identified 100-mer to map the epitope of interest.

The polypeptides described herein can be produced recombinantly. A polynucleotide encoding a polypeptide described herein can be introduced into a recombinant expression vector, which can be expressed in a suitable expression host cell system using techniques well known in

the art. A variety of bacterial, yeast, plant, mammalian, and insect expression systems are available in the art and any such expression system can be used. Optionally, a polynucleotide encoding a polypeptide can be translated in a cell-free translation system. A polypeptide can also be chemically synthesized or obtained from *Anaplasma platys* cells.

For example, and not to be limiting, an immunogenic polypeptide of the invention can comprise an amino acid sequence shown in SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or fragments thereof. An immunogenic polypeptide can elicit antibodies or other immune responses (e.g., T-cell responses of the immune system) that recognize epitopes of a polypeptide having SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or fragments thereof. An immunogenic polypeptide of the invention can also be a fragment of a polypeptide that has an amino acid sequence shown in SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or fragments thereof. An immunogenic polypeptide fragment of the invention can be about 10, 15, 20, 25, 30, 40, 50 or more amino acids in length.

Polypeptide Production

Polypeptides that can be used in the disclosed methods can be produced by any method known in the art. One method of producing the disclosed polypeptides is to link two or more amino acid residues, peptides or polypeptides together by protein chemistry techniques. For example, peptides or polypeptides are chemically synthesized using currently available laboratory equipment using either Fmoc (9-fluorenylmethyloxycarbonyl) or Boc (tert-butyloxycarbonyl) chemistry (Applied Biosystems, Inc., Foster City, Calif.). A peptide or polypeptide can be synthesized and not cleaved from its synthesis resin, whereas the other fragment

of a peptide or protein can be synthesized and subsequently cleaved from the resin, thereby exposing a terminal group, which is functionally blocked on the other fragment. By peptide condensation reactions, these two fragments can be covalently joined via a peptide bond at their carboxyl and amino termini, respectively, (Grant G A (1992) *Synthetic Peptides: A User Guide*, W.H. Freeman and Co., N.Y. (1992); Bodansky M and Trost B., Ed. (1993) *Principles of Peptide Synthesis*, Springer-Verlag Inc., NY). Alternatively, the peptide or polypeptide is independently synthesized in vivo. Once isolated, these independent peptides or polypeptides can be linked to form a peptide or fragment thereof via similar peptide condensation reactions.

For example, enzymatic ligation of cloned or synthetic peptide segments allow relatively short peptide fragments to be joined to produce larger peptide fragments, polypeptides or whole protein domains (Abrahamsen L et al., *Biochemistry*, 30:4151 (1991)). Alternatively, native chemical ligation of synthetic peptides can be utilized to synthetically construct large peptides or polypeptides from shorter peptide fragments. This method consists of a two-step chemical reaction (Dawson et al. *Science*, 266:776-779 (1994)). The first step is the chemoselective reaction of an unprotected synthetic peptide-thioester with another unprotected peptide segment containing an amino-terminal Cys residue to give a thioester-linked intermediate as the initial covalent product. Without a change in the reaction conditions, this intermediate undergoes spontaneous, rapid intramolecular reaction to form a native peptide bond at the ligation site (Baggiolini M et al. (1992) *FEBS Lett.* 307:97-101; Clark-Lewis I et al., *J. Biol. Chem.*, 269:16075 (1994); Clark-Lewis I et al., *Biochem.*, 30:3128 (1991); Rajarathnam K et al., *Biochem.* 33:6623-30 (1994)).

Alternatively, unprotected peptide segments are chemically linked where the bond formed between the peptide segments as a result of the chemical ligation is an unnatural (non-peptide) bond (Schnolzer, M et al. *Science*, 256:221 (1992)). This technique has been used to synthesize analogs of protein domains as well as large amounts of relatively pure proteins with full biological activity (deLisle Milton R C et al., *Techniques in Protein Chemistry IV*, Academic Press, New York, pp. 257-267 (1992)).

Also disclosed are the components to be used to prepare the disclosed *A. platys* peptides that can be used in the disclosed methods as well as the compositions themselves to be used within the methods disclosed herein. These and other materials are disclosed herein, and it is understood that when combinations, subsets, interactions, groups, etc. of these materials are disclosed that while specific reference of each various individual and collective combinations and permutation of these compounds may not be explicitly disclosed, each is specifically contemplated and described herein. For example, if a particular polynucleotide is disclosed and discussed and a number of modifications that can be made to a number of molecules including the polynucleotide are discussed, specifically contemplated is each and every combination and permutation of polynucleotide and the modifications that are possible unless specifically indicated to the contrary. Thus, if a class of molecules A, B, and C are disclosed as well as a class of molecules D, E, and F and an example of a combination molecule, A-D is disclosed, then even if each is not individually recited each is individually and collectively contemplated meaning combinations, A-E, A-F, B-D, B-E, B-F, C-D, C-E, and C-F are considered disclosed. Likewise, any subset or combination of these is also disclosed. Thus, for example, the sub-group of A-E, B-F, and C-E would be considered disclosed. This

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concept applies to all aspects of this application including, but not limited to, steps in methods of making and using the disclosed compositions. Thus, if there are a variety of additional steps that can be performed it is understood that each of these additional steps can be performed with any specific embodiment or combination of embodiments of the disclosed methods.

It is understood that one way to define any known variants and derivatives or those that might arise, of the disclosed genes and proteins herein is through defining the variants and derivatives in terms of homology to specific known sequences. Specifically disclosed are variants of the genes and proteins herein disclosed which have at least, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent homology to the stated sequence. Those of skill in the art readily understand how to determine the homology of two proteins or nucleic acids, such as genes. For example, the homology can be calculated after aligning the two sequences so that the homology is at its highest level.

Antibodies

Described herein are isolated or purified antibodies that selectively hybridize to a peptide chosen from: *Anaplasma platys* P44 protein, *Anaplasma platys* OMP-1X protein, P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof. In one aspect, the antibodies described herein can hybridize to a peptide chosen from one or more of: P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19, the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ

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ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof. In a further aspect, the antibodies described herein can hybridize to one or more of a peptide that is at least 95% identical to the P44 or OMP-1X peptide sequences described herein. In a further aspect, the antibodies described herein can hybridize to one or more of a variant or antigenic fragment of the P44 or OMP-1X peptide sequences described herein. In still a further aspect, the antibodies described herein can hybridize to one or more of a variant or antigenic fragment of a peptide that is at least 95% identical to the P44 or OMP-1X peptide sequences described herein.

Disclosed herein are antibodies that specifically and stably bind to an *Anaplasma platys* p44 polypeptide, an *Anaplasma platys* OMP-1X peptide, or fragment thereof. Antibodies can also specifically and stably bind to an *Anaplasma platys* P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6 polypeptide or fragment thereof. Antibodies can also specifically and stably bind to an *Anaplasma platys* OMP-1X Box 1 polypeptide, an OMP-1X Box 2 polypeptide or fragment thereof. One of skill in the art can easily determine if an antibody is specific for an *Anaplasma platys* polypeptide using assays described herein. An antibody can be a polyclonal antibody, a monoclonal antibody, a single chain antibody (scFv), or an antigen binding fragment of an antibody. Antigen-binding fragments of antibodies are a portion of an intact antibody comprising the antigen binding site or variable region of an intact antibody, wherein the portion is free of the constant heavy chain domains of the Fc region of the intact antibody. Examples of antibody fragments include Fab, Fab', Fab'-SH, F(ab')₂ and F_v fragments.

The antibodies described herein can be any antibody class, including for example, IgG, IgM, IgA, IgD and IgE. An antibody or fragment thereof binds to an epitope of a polypeptide of the invention. An antibody can be made in vivo in suitable laboratory animals or in vitro using recombinant DNA techniques. Means for preparing and characterizing antibodies are well known in the art. See, e.g., Dean, Methods Mol. Biol. 80:23-37 (1998); Dean, Methods Mol. Biol. 32:361-79 (1994); Baileg, Methods Mol. Biol. 32:381-88 (1994); Gullick, Methods Mol. Biol. 32:389-99 (1994); Drenckhahn et al. Methods Cell. Biol. 37:7-56 (1993); Morrison, Ann. Rev. Immunol. 10:239-65 (1992); Wright et al. Crit. Rev. Immunol. 12:125-68 (1992). For example, polyclonal antibodies can be produced by administering a polypeptide of the invention to an animal, such as a human or other primate, mouse, rat, rabbit, guinea pig, goat, pig, dog, cow, sheep, donkey, or horse. Serum from the immunized animal is collected and the antibodies are purified from the plasma by, for example, precipitation with ammonium sulfate, followed by chromatography, such as affinity chromatography. Techniques for producing and processing polyclonal antibodies are known in the art.

"Specifically binds" or "specific for" means that a first antigen, e.g., an *Anaplasma platys* polypeptide, recognizes and binds to an antibody of the invention with greater affinity than other, non-specific molecules. A non-specific molecule is an antigen that shares no common epitope with the first antigen. In this case, *Anaplasma platys* polypeptides would not generally be desirable choices for non-specific control molecules. For example, an antibody raised against a first antigen (e.g., a polypeptide) to which it binds more efficiently than to a non-specific antigen can be described as specifically binding to the first antigen. In a preferred embodiment, an antibody or antigen-binding portion thereof specifically binds to a polypeptide of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or fragments thereof. Specific binding can be tested using, for example, an enzyme-linked immunosorbent assay (ELISA), a radioimmunoassay (RIA), or a western blot assay using methodology well known in the art.

Additionally, monoclonal antibodies directed against epitopes present on a polypeptide of the invention can also be readily produced. For example, normal B cells from a mammal, such as a mouse, which was immunized with a polypeptide of the invention can be fused with, for example, HAT-sensitive mouse myeloma cells to produce hybridomas. Hybridomas producing *Anaplasma platys*-specific antibodies can be identified using RIA or ELISA and isolated by cloning in semi-solid agar or by limiting dilution. Clones producing *Anaplasma platys*-specific antibodies are isolated by another round of screening. Monoclonal antibodies can be screened for specificity using standard techniques, for example, by binding a polypeptide of the invention to a microtiter plate and measuring binding of the monoclonal antibody by an ELISA assay. Techniques for producing and processing monoclonal antibodies are known in the art. See e.g., Kohler & Milstein, *Nature*, 256:495 (1975). Particular isotypes of a monoclonal antibody can be prepared directly, by selecting from the initial fusion, or prepared secondarily, from a parental hybridoma secreting a monoclonal antibody of a different isotype by using a sib selection technique to isolate class-switch variants. See Steplewski et al., *P.N.A.S. U.S.A.* 82:8653 1985; Spria et al., *J. Immunolog. Meth.* 74:307, 1984. Monoclonal antibodies of the invention can also be recombinant monoclonal antibodies. See, e.g., U.S. Pat. Nos. 4,474,893; 4,816,567. Antibodies of the invention can also be chemically constructed. See, e.g., U.S. Pat. No. 4,676,980.

Antibodies can be chimeric (see, e.g., U.S. Pat. No. 5,482,856), humanized (see, e.g., Jones et al., *Nature* 321: 522 (1986); Reichmann et al., *Nature* 332:323 (1988); Presta, *Curr. Op. Struct. Biol.* 2:593 (1992)), caninized, canine, or human antibodies. Human antibodies can be made by, for example, direct immortalization, phage display, transgenic mice, or a Trimeria methodology, see e.g., Reisener et al., *Trends Biotechnol.* 16:242-246 (1998).

Antibodies that specifically bind *Anaplasma platys* antigens (e.g., *Anaplasma platys* polypeptides), are particularly

useful for detecting the presence of Apl or Apl antigens in a sample, such as a serum, blood, plasma, urine, fecal, or saliva sample from an Apl- or Aph-infected animal. An immunoassay for *Anaplasma platys* antigen can utilize one antibody or several antibodies. An immunoassay for *Anaplasma platys* antigen can use, for example, a monoclonal antibody specific for an *Anaplasma platys* epitope, a combination of monoclonal antibodies specific for epitopes of one *Anaplasma platys* polypeptide, monoclonal antibodies specific for epitopes of different *Anaplasma platys* polypeptides, polyclonal antibodies specific for the same *Anaplasma platys* antigen, polyclonal antibodies specific for different *Anaplasma platys* antigens, or a combination of monoclonal and polyclonal antibodies. Immunoassay protocols can be based upon, for example, competition, direct reaction, or sandwich type assays using, for example, labeled antibody. Antibodies can be labeled with any type of label known in the art, including, for example, fluorescent, chemiluminescent, radioactive, enzyme, colloidal metal, radioisotope and bioluminescent labels.

Antibodies or fragments thereof can be bound to a support and used to detect the presence of *Anaplasma platys* antigen. Supports include, for example, glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and maglite.

Antibodies can further be used to isolate *Anaplasma platys* organisms or *Anaplasma platys* antigens by immunoaffinity columns. The antibodies can be affixed to a solid support by, for example, adsorption or by covalent linkage so that the antibodies retain their immunoselective activity. Optionally, spacer groups can be included so that the antigen binding site of the antibody remains accessible. The immobilized antibodies can then be used to bind *Anaplasma platys* organisms or *Anaplasma platys* antigens from a sample, such as a biological sample including saliva, serum, sputum, blood, urine, feces, cerebrospinal fluid, amniotic fluid, wound exudate, or tissue. The bound *Anaplasma platys* organisms or *Anaplasma platys* antigens are recovered from the column matrix by, for example, a change in pH.

Antibodies can also be used in immunolocalization studies to analyze the presence and distribution of a polypeptide of the invention during various cellular events or physiological conditions. Antibodies can also be used to identify molecules involved in passive immunization and to identify molecules involved in the biosynthesis of non-protein antigens. Identification of such molecules can be useful in vaccine development. Antibodies, including, for example, monoclonal antibodies and single chain antibodies, can be used to monitor the course of amelioration of a disease caused by *Anaplasma platys*. By measuring the increase or decrease of *Anaplasma platys* antibodies to *Anaplasma platys* antigens in a test sample from an animal, it can be determined whether a particular therapeutic regiment aimed at ameliorating the disorder is effective. Antibodies can be detected and/or quantified using for example, direct binding assays such as RIA, ELISA, or western blot assays.

In one aspect, the antibodies can be immunoglobulin molecules that specifically and stably bind to *A. platys* P44 or OMP-1X polypeptide or fragment thereof. In a further aspect, the antibody can be monoclonal, polyclonal, or a single chain antibody. In yet a further aspect, an antibody can be an antigen-binding fragments, which is a portion of an intact antibody comprising the antigen binding site or variable region of an intact antibody, wherein the portion is free of the constant heavy chain domains of the Fc region of the intact antibody.

In one aspect, monoclonal antibodies directed against epitopes present on a polypeptide discussed herein can be produced. In a further aspect, clones producing *A. platys*-specific antibodies can be isolated via additional screening. In yet a further aspect, monoclonal antibodies can also be recombinant monoclonal antibodies. Monoclonal antibodies can be screened for specificity using standard techniques known in the art.

In one aspect, an antibody can belong to any antibody class. In a further aspect, an antibody or fragment thereof can bind to an epitope of a polypeptide disclosed herein. An antibody can be made in vivo in suitable laboratory animals or in vitro via recombinant DNA techniques known in the art.

Means for preparing and characterizing antibodies are well known in the art. For example, polyclonal antibodies can be produced by administering a polypeptide described herein to an animal, such as a human or other primate, mouse, rat, rabbit, dog, cow, sheep, or horse. Serum from the immunized animal can be collected and the antibodies can be purified from the plasma.

In one aspect, antibodies can be chimeric, canine, or human antibodies. In a further aspect, antibodies or fragments thereof can be bound to a support. Supports can include, glass, polystyrene, polypropylene, polyethylene, nylon, celluloses, or polyacrylamides.

Vaccines

In one aspect, described herein are *Anaplasma platys* P44 protein based vaccines. Thus, described herein are peptides comprising one or more amino-acid sequences selected from the group consisting of P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19, the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about

position 416 to about position 433 of FIG. 19, or a fragment thereof. In a further aspect, the peptides disclosed herein can comprise one or more amino-acid sequences selected from the group consisting of a combination of any P44 peptide sequences described herein.

In yet a further aspect, the vaccines described herein can comprise one or more amino-acid sequences selected from the group consisting of a variant of the P44 proteins described herein, or an antigenic fragment of the P44 proteins described herein. In still a further aspect, the vaccines described herein can comprise one or more amino-acid sequences selected from the group consisting of a sequence that is at least 95% identical to a P44 protein, a variant of the P44 protein, or an antigenic fragment of the P44 protein sequences described herein. The peptides described herein can also be any antigenically related variant of the peptide sequences which have an identity of 95% and are capable of immunologically mimicking the corresponding antigenic determinant site of the P44 protein of *Anaplasma platys*.

In one aspect, the vaccines described herein can be *Anaplasma platys* OMP-1X protein based vaccines. Thus, described herein are peptides comprising one or more amino-acid sequences selected from the group consisting of OMP-1X Box 1, OMP-1X Box 2, SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof. In a further aspect, the peptides disclosed herein can comprise one or more amino-acid sequences selected from the group consisting of a combination of any OMP-1X peptide sequences described herein.

In yet a further aspect, the vaccines described herein can comprise one or more amino-acid sequences selected from the group consisting of a variant of the OMP-1X proteins described herein, or an antigenic fragment of the OMP-1X proteins described herein. In still a further aspect, the vaccines described herein can comprise one or more amino-acid sequences selected from the group consisting of a sequence that is at least 95% identical to a OMP-1X protein, a variant of the OMP-1X protein, or an antigenic fragment of the OMP-1X protein sequences described herein. The peptides described herein can also be any antigenically related variant of the peptide sequences which have an identity of 95% and are capable of immunologically mimicking the corresponding antigenic determinant site of the OMP-1X protein of *Anaplasma platys*. Antigenically related variants can have amino acids added, inserted, substituted or deleted.

Furthermore, described herein are chimeric peptides comprising: one or more *Anaplasma platys* P44 proteins or *Anaplasma platys* OMP-1X proteins described herein; one or more variants of the *Anaplasma platys* P44 proteins or *Anaplasma platys* OMP-1X proteins described herein; one or more antigenic fragments of the *Anaplasma platys* P44 proteins or *Anaplasma platys* OMP-1X proteins described

herein; or one or more proteins that are at least 95% identical to the *Anaplasma platys* P44 proteins or *Anaplasma platys* OMP-1X proteins described herein, linked to a carrier polypeptide that can comprise at least one T-cell epitope. In one aspect, the chimeric peptides described herein can further comprise a purification tag peptide sequence. For example, and not to be limiting, the purification tag sequence can be a Histidine-tag sequence. Also disclosed herein are purified antibodies that are immunospecific to the chimeric peptides described herein. In one aspect, a purification tag peptide sequence (such as a Histidine tag or a Glutathione-S-transferase tag) can be used in order to aid subsequent purification of the polypeptide. Optional short peptide spacer sequences can be introduced between elements of the chimeric polypeptide. When one is required a Histidine tag sequence can be located at the C-terminus of the polypeptide.

Further described herein are vaccine compositions comprising an immunogenic amount of at least: one *Anaplasma platys* P44 protein or *Anaplasma platys* OMP-1X protein described herein; one variant of the *Anaplasma platys* P44 proteins or *Anaplasma platys* OMP-1X proteins described herein; one antigenic fragment of the *Anaplasma platys* P44 proteins or *Anaplasma platys* OMP-1X proteins described herein; or one protein that is at least 95% identical to the *Anaplasma platys* P44 proteins or *Anaplasma platys* OMP-1X proteins described herein, wherein the protein or peptide can be in a pharmaceutically acceptable excipient, and an optional adjuvant. Vaccine preparation is generally described in Vaccine Design ("The subunit and adjuvant approach" (eds. Powell M. F. & Newman M. J.). (1995) Plenum Press New York), which is hereby incorporated in its entirety by this reference. Suitable adjuvants include, but are not limited to an aluminium salt such as aluminium hydroxide gel (alum) or aluminium phosphate, but can also be a salt of calcium, iron or zinc, or can be an insoluble suspension of acylated tyrosine, or acylated sugars, cationically or anionically derivatised polysaccharides, or polyphosphazenes. Other known adjuvants include CpG containing oligonucleotides. The oligonucleotides can be characterized in that the CpG dinucleotide is unmethylated. Such oligonucleotides are well known in the art and are described in, for example WO96/02555. In one aspect, the adjuvants can induce an immune response, for example, of the TH1 type. High levels of Th1-type cytokines can favor the induction of cell mediated immune responses to the given antigen, while high levels of Th2-type cytokines can favor the induction of humoral immune responses to the antigen. Suitable adjuvant systems can include, for example, monophosphoryl lipid A, 3-de-O-acylated monophosphoryl lipid A (3D-MPL), or a combination of 3D-MPL together with an aluminium salt. CpG oligonucleotides can also induce a TH1 response. An enhanced system can involve the combination of a monophosphoryl lipid A and a saponin derivative, for example, the combination of QS21 and 3D-MPL as disclosed in WO 94/00153, or a less reactogenic composition where the QS21 can be quenched with cholesterol as described in WO 96/33739. Another adjuvant formulation involving QS21 3D-MPL & tocopherol in an oil in water emulsion is described in WO 95/17210.

Also described herein are methods of inducing an immune response in a mammal susceptible to *Anaplasma platys* infection comprising administering to the mammal an effective amount of the vaccine compositions described herein. As used herein, "infection" can also mean "exposure," and the terms can be used interchangeably.

Additionally, described herein are methods of preventing *Anaplasma platys* infection comprising administering to a mammal an effective amount of the vaccine compositions described herein.

5 Vectors

Also described herein are vectors for transformation of a host cell comprising an isolated polynucleotide that can encode an outer membrane protein of *Anaplasma platys*, a variant of said outer membrane protein, or an immunogenic fragment of said outer membrane protein. In one aspect, the outer membrane protein can be the P44 protein, P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, OMP-1X protein, OMP-1X Box 1, OMP-1X Box 2, OMP-1X Box 1 and OMP-1X Box 2, or a fragment thereof. The vectors disclosed herein can comprise any of the isolated polynucleotide sequences disclosed or described herein.

The polynucleotides described herein can comprise coding sequences for naturally occurring polypeptides or can encode altered sequences that do not occur in nature. If desired, polynucleotides can be cloned into an expression vectors comprising expression control elements, including for example, origins of replication, promoters, enhancers, or other regulatory elements that drive expression of the polynucleotides of the invention in host cells. An expression vector can be, for example, a plasmid, such as pBR322, pUC, or ColE1, or an adenovirus vector, such as an adenovirus Type 2 vector or Type 5 vector. Optionally, other vectors can be used, including but not limited to Sindbis virus, simian virus 40, alphavirus vectors, poxvirus vectors, and cytomegalovirus and retroviral vectors, such as murine sarcoma virus, mouse mammary tumor virus, Moloney murine leukemia virus, and Rous sarcoma virus. Minichromosomes such as MC and MC1, bacteriophages, phagemids, yeast artificial chromosomes, bacterial artificial chromosomes, virus particles, virus-like particles, cosmids (plasmids into which phage lambda cos sites have been inserted) and replicons (genetic elements that are capable of replication under their own control in a cell) can also be used.

Methods for preparing polynucleotides operably linked to an expression control sequence and expressing them in a host cell are well-known in the art. See, e.g., U.S. Pat. No. 4,366,246. A polynucleotide of the invention is operably linked when it is positioned adjacent to or close to one or more expression control elements, which direct transcription and/or translation of the polynucleotide.

In a further aspect, the vectors described herein can be used in a process for making a corresponding outer membrane protein of *Anaplasma platys*, a variant of said outer membrane protein, or an immunogenic fragment of said outer membrane protein. For example, and not to be limiting, the process can comprise transfecting host cells with any of the vectors described herein and inducing expression of the outer membrane protein or the variant or immunogenic fragment thereof in any of the host cells described herein.

Expression vectors for production of proteins and peptides are well known in the art (see Ausubel et al., 2004, Current Protocols In Molecular Biology, Greene Publishing and Wiley-Interscience, New York). Such expression vectors can include the nucleic acid sequence encoding the *Anaplasma platys* polypeptides linked to regulatory elements, such as a promoter, which drives transcription of the DNA and can be adapted for expression in prokaryotic (e.g., *E. coli*) and eukaryotic (e.g., yeast, insect or mammalian cells) hosts. A variant *Anaplasma platys* polypeptide can also be expressed in an expression vector in which a variant *Anaplasma platys* gene is operably linked to a promoter. The

promoter can be a eukaryotic promoter for expression in a mammalian cell. The transcription regulatory sequences can comprise a heterologous promoter and optionally an enhancer, which is recognized by the host cell. Commercially available expression vectors can also be used. Expression vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

Host Cells

Also disclosed herein are host cells comprising any of the vectors disclosed or described herein. Suitable host cells can include, but are not limited to, bacteria such as *E. coli*, yeast, filamentous fungi, mollusk cells, snail cells, insect cells, and mammalian cells, which are typically immortalized, including mouse, hamster, human, and monkey cell lines, and derivatives thereof. Host cells may be able to process the *Anaplasma platys* gene product to produce an appropriately processed, mature polypeptide. Such processing can include glycosylation, ubiquitination, disulfide bond formation, and the like.

Kits

Described herein are kits for diagnosing *Anaplasma platys* in a subject, wherein the kit can comprise the *Anaplasma platys* P44 protein, an antigenic fragment of the *Anaplasma platys* P44 protein, or both. In one aspect, in the kits disclosed herein, the protein can comprise: one or more *Anaplasma platys* P44 proteins described herein; one or more variants of the *Anaplasma platys* P44 proteins described herein; one or more antigenic fragments of the *Anaplasma platys* P44 proteins described herein; or one or more proteins that are at least 95% identical to the *Anaplasma platys* P44 proteins described herein.

Also described herein are kits for diagnosing *Anaplasma platys* in a subject, wherein the kit can comprise the *Anaplasma platys* OMP-1X protein, an antigenic fragment of the *Anaplasma platys* OMP-1X protein, or both. In one aspect, in the kits disclosed herein, the protein can comprise: one or more *Anaplasma platys* OMP-1X proteins described herein; one or more variants of the *Anaplasma platys* OMP-1X proteins described herein; one or more antigenic fragments of the *Anaplasma platys* OMP-1X proteins described herein; or one or more proteins that are at least 95% identical to the *Anaplasma platys* OMP-1X proteins described herein.

Further described herein are kits for diagnosing *Anaplasma platys* in a subject comprising one or more of the antibodies described herein. In one aspect, the kits described herein can further comprise a biomolecule for detecting an interaction between the reagent and antibodies in a sample from an animal.

Also described herein are reagent kits for diagnosing infection or exposure with *Anaplasma platys* in a subject comprising a DNA probe or primer constructed to correspond to the P44 protein, P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, or P44 Box 6 of *Anaplasma platys*, characterized in that the probe or primer comprises one or more of the nucleotides or polynucleotides described herein.

Also described herein are reagent kits for diagnosing infection or exposure with *Anaplasma platys* in a subject comprising a DNA probe or primer constructed to correspond to the OMP-1X protein, OMP-1X Box 1, or OMP-1X Box 2 of *Anaplasma platys*, characterized in that the probe or primer comprises one or more of the nucleotides or polynucleotides described herein.

The kits described herein can comprise one or more of the polypeptides described herein and means for determining binding of the polypeptide to anti-*Anaplasma platys* or antibody fragments in the sample. A kit or article of manu-

facture can also comprise one or more antibodies or antibody fragments described herein and means for determining binding of the antibodies or antibody fragments to *Anaplasma platys* and/or *Anaplasma platys* polypeptides in the sample. A kit can comprise a device containing one or more polypeptides or antibodies described herein and instructions for use of the one or more polypeptides or antibodies for, e.g., the identification of an *Anaplasma platys* infection in a mammal. The kit can also comprise packaging material comprising a label that indicates that the one or more polypeptides or antibodies of the kit can be used for the identification of *Anaplasma platys* infection. Other components such as buffers, controls, and the like, known to those of ordinary skill in art, can be included in such test kits. The polypeptides, antibodies, assays, and kits of the invention are useful, for example, in the diagnosis of individual cases of *Anaplasma platys* infection in a subject, as well as epidemiological studies of *Anaplasma platys* outbreaks. Exposure to *Anaplasma platys* can also be detected. Exposure would include the presence of *Anaplasma platys* organisms without clinical symptoms and prior infection with *Anaplasma platys*.

Samples

Vertebrate host samples are collected from body tissue or bodily fluid, such as for example, blood, plasma, saliva, and peripheral blood mononuclear cells. For the invertebrate vectors which can transmit the pathogen from one vertebrate host to another, the sample can be from dissected ticks (e.g., midgut, salivary glands, and hemolymph), tick pieces, and frozen and smashed ticks in preparation for PCR assays. Further preparation of tick tissues can involve heating the sample, digesting the samples with proteases, and isolating pure DNA from the tick tissues. Other suitable samples include, but are not limited to, saliva, cheek scrapings, biopsies of retina, kidney or liver or other organs or tissues; skin biopsies; amniotic fluid; or CNS samples; and the like.

Methods

PCR Based Diagnostics

Described herein are methods for detecting *Anaplasma platys* in a sample obtained from a subject, comprising (a) providing a primer set comprising: (i) one or more forward primers comprising the sequence of: SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO:84, or SEQ ID NO: 90 and (ii) one or more reverse primers comprising the sequence of: SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO:88, SEQ ID NO: 89 or SEQ ID NO: 91; (b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and (c) determining the length or sequence of the PCR products of step (b), wherein the presence of a PCR product having a length or sequence which corresponds to the length or sequence, respectively, of that region of the *Anaplasma platys* p44 gene which is located between the regions to which the one or more forward primers and the one or more reverse primers bind is indicative of the presence of *Anaplasma platys* in the sample. For example, and not to be limiting, the one or more forward or reverse primers can be from 15 to 35 nucleotides in length. In one aspect, the forward and the reverse primer can comprise SEQ ID NO: 90 and SEQ ID NO: 91, respectively.

Further described herein are primer sets for detecting *Anaplasma platys* in a sample, the primer set comprising: (a) one or more forward primers comprising the sequence of: SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO:84, or SEQ ID NO: 90 and (ii) one or more reverse primers comprising

the sequence of: SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89 or SEQ ID NO: 91. For example, and not to be limiting, the one or more forward or reverse primers can be from 15 to 35 nucleotides in length. In one aspect, the forward and the reverse primer can comprise SEQ ID NO: 90 and SEQ ID NO: 91, respectively.

Also described herein are methods for detecting *Anaplasma platys* in a sample obtained from a subject, comprising (a) providing a primer set comprising: (i) one or more forward primers comprising the sequence of: SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, or SEQ ID NO: 62 and (ii) one or more reverse primers comprising the sequence of: SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, or SEQ ID NO: 63; (b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and (c) determining the length or sequence of the PCR products of step (b), wherein the presence of a PCR product having a length or sequence which corresponds to the length or sequence, respectively, of that region of the *Anaplasma platys* p44 gene which is located between the regions to which the one or more forward primers and the one or more reverse primers bind is indicative of the presence of *Anaplasma platys* in the sample. For example, and not to be limiting, the one or more forward or reverse primers can be from 15 to 35 nucleotides in length. In one aspect, the forward and the reverse primer can comprise one or more of pairs of sequences described herein, including, but not limited to: PAIR 1: SEQ ID NO: 52 and SEQ ID NO: 53; PAIR 2: SEQ ID NO: 54 and SEQ ID NO: 55; PAIR 3: SEQ ID NO: 56 and SEQ ID NO: 57; PAIR 4: SEQ ID NO: 58 and SEQ ID NO: 59; PAIR 5: SEQ ID NO: 60 and SEQ ID NO: 61; or PAIR 6: SEQ ID NO: 62 and SEQ ID NO: 63.

Further described herein are primer sets for detecting *Anaplasma platys* in a sample, the primer set comprising: (a) one or more forward primers comprising the sequence of: SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, or SEQ ID NO: 90 and (ii) one or more reverse primers comprising the sequence of: SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89 or SEQ ID NO: 91. For example, and not to be limiting, the one or more forward or reverse primers can be from 15 to 35 nucleotides in length.

Described herein are methods for detecting *Anaplasma platys* in a sample obtained from a subject, comprising (a) providing a primer set comprising: (i) one or more forward primers comprising the sequence of: SEQ ID NO: 64, SEQ ID NO: 18, or SEQ ID NO: 20 and (ii) one or more reverse primers comprising the sequence of: SEQ ID NO: 65, SEQ ID NO: 19, or SEQ ID NO: 99; (b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and (c) determining the length or sequence of the PCR products of step (b), wherein the presence of a PCR product having a length or sequence which corresponds to the length or sequence, respectively, of that region of the *Anaplasma platys* OMP-1X gene which is located between the regions to which the one or more forward primers and the one or more reverse primers bind is indicative of the presence of *Anaplasma platys* in the sample. For example, and not to be limiting, the one or more forward or reverse primers can be from 15 to 35 nucleotides in length. In one aspect, the forward and reverse primers can comprise one or more pairs of sequences described herein, including, but not limited to: PAIR 1: SEQ ID NO: 64 and SEQ ID NO: 65; PAIR 2: SEQ ID NO: 18 and SEQ ID NO: 19; or PAIR 3: SEQ ID NO: 20 and SEQ ID NO: 99, respectively.

Further described herein are primer sets for detecting *Anaplasma platys* in a sample, the primer set comprising: (a) one or more forward primers comprising the sequence of: SEQ ID NO: 64, SEQ ID NO: 18, or SEQ ID NO: 20 and (ii) one or more reverse primers comprising the sequence of: SEQ ID NO: 65, SEQ ID NO: 19, or SEQ ID NO: 99. For example, and not to be limiting, the one or more forward or reverse primers can be from 15 to 35 nucleotides in length.

Also described herein are methods of detecting the presence of *Anaplasma platys* in a sample by contacting the sample with a DNA probe or primer constructed to correspond to the P44 protein of *Anaplasma platys*, characterized in that the probe or primer comprises one or more of the nucleotides or polynucleotides described herein.

Further described herein are methods of detecting the presence of *Anaplasma platys* in a sample by contacting the sample with a DNA probe or primer constructed to correspond to the OMP-1X protein, OMP-1X Box 1, or OMP-1X Box 2 of *Anaplasma platys*, characterized in that the probe or primer comprises one or more of the nucleotides or polynucleotides described herein.

PCR assays are well known in the art, including, for example, U.S. Pat. Nos. 4,683,195; 4,683,202; 4,965,188. Generally, polynucleotide primers are annealed to denatured strands of a target nucleic acid. Primer extension products are formed by polymerization of deoxynucleoside triphosphates by a polymerase. PCR then involves repetitive cycles of template nucleic acid denaturation, primer annealing and extension of the annealed primers by the action of a thermostable polymerase. The process results in exponential amplification of the target *Anaplasma platys* nucleic acids in the test sample, which allows for the detection of target polynucleotides existing in very low concentrations in a sample.

Real-time PCR assays are based on the detection of a signal, e.g., a fluorescent reporter signal. This signal increases in direct proportion to the amount of PCR product in a reaction. Real-time PCR is any amplification technique that makes it possible to monitor the evolution of an ongoing amplification reaction. See, Quantitation of DNA/RNA Using Real-Time PCR Detection, Perkin Elmer Applied Biosystems (1999); PCR Protocols (Academic Press New York, 1989). By recording the amount of fluorescence emission at each cycle, it is possible to monitor the PCR reaction during exponential phase where the first significant increase in the amount of PCR product correlates to the initial amount of target template. The higher the starting copy number of the nucleic acid target, the sooner a significant increase in fluorescence is observed.

Described herein are methods for detecting and/or quantifying *Anaplasma platys* polynucleotides in a test sample. Sense primers and antisense primers can be added to a test sample under conditions suitable for a polymerase chain reaction. The primers hybridize with *Anaplasma platys* P44 or OMP-1X polynucleotides such that an amplification product is formed if *Anaplasma platys* P44 or OMP-1X polynucleotides are present in the test sample. In one aspect, the primers can be SEQ ID NOs: 90 and 91. Amplification products are detected and the presence and/or quantity of *Anaplasma platys* P44 or OMP-1X polynucleotides is determined. Amplification products can be detected with a polynucleotide probe that hybridizes, under conditions suitable for a polymerase chain reaction, with an *Anaplasma platys* P44 or OMP-1X polynucleotide sequence. Examples of probes include SEQ ID NOs: 17 which can be used to identify the presence of an OMP-1X polynucleotide. The amplification product can be quantified by measuring a

detection signal from the probe and comparing said detection signal to a second probe detection signal from a quantification standard. The quantification standard can be extracted in parallel with the test sample.

Also disclosed are methods wherein the PCR primers can be selected from the variable regions of an *Anaplasma platys* P44 or OMP-1X polynucleotide. For example, primers of 10, 15, 20, 25, 30, or 40 contiguous nucleotides can be selected from the regions of P44 Boxes 1-6 or OMP-1X Boxes 1 or 2.

The polynucleotides described herein can be used to detect the presence of *Anaplasma platys* polynucleotides in a sample. The polynucleotides can be used to detect *Anaplasma platys* polynucleotides in a sample by a simple hybridization reaction and can also be used in, e.g., polymerase chain reactions (PCR) such as a real-time PCR reaction. The methods and compositions described herein can also be used to differentially detect the presence *Anaplasma platys* from *Anaplasma phagocytophilum* or other *Anaplasma* species.

Antibody Based Diagnostics

Also described herein are methods for detecting *Anaplasma platys* in a sample by contacting the sample with one or more of the antibodies described herein. In one aspect, to the *Anaplasma platys* in a sample of a bodily fluid from a patient. The method comprises providing an isolated outer membrane protein of *Anaplasma platys*, for example, a recombinant form of the isolated protein, contacting the outer membrane protein or polypeptide with a sample taken from the patient; and assaying for the formation of a complex between the outer membrane protein or polypeptide and antibodies in the sample. In one aspect, the isolated protein or polypeptide be attached to a substrate such as a column, plastic dish, matrix, or membrane, preferably nitrocellulose. The sample can be a tissue or a biological fluid, including urine, whole blood, exudate, or serum. The sample can be untreated, subjected to precipitation, fractionation, separation, or purification before combining with the isolated protein or peptide. Interactions between antibodies in the sample and the isolated protein or peptide can be detected by radiometric, colorimetric, or fluorometric means, size-separation, or precipitation. In one aspect, detection of the antibody-outer membrane protein complex can be by addition of a secondary antibody that can be coupled to a detectable tag, such as for example, an enzyme, fluorophore, or chromophore. Formation of the complex is indicative of the presence of anti-*Anaplasma platys* antibodies, either IgM or IgG, in the patient. Thus, the method can be used to determine whether a subject is infected with *Anaplasma platys*.

In one aspect, the method can employ an enzyme-linked immunosorbent assay (ELISA) or a Western immunoblot procedure. Such methods can be relatively simple to perform and do not require special equipment as long as membrane strips are coated with a high quality antigen. Accordingly, in one aspect, it can be advantageous to use a recombinant form of the outer membrane protein of *Anaplasma platys* since such proteins, typically, are more pure and consistent in quality than a purified form of such protein.

Peptide Based Diagnostics

Described herein are methods of detecting antibodies that specifically bind an *Anaplasma platys* polypeptide, comprising: (a) contacting a purified polypeptide comprising the amino acid sequence of one or more of the following: (i) P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof; (ii) a variant of P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6,

or a fragment thereof; (iii) an antigenic fragment of P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof; (iv) SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, or a fragment thereof; (v) a variant of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, or a fragment thereof; (vi) an antigenic fragment of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, or SEQ ID NO: 45; (vii) SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, or a fragment thereof; (viii) a variant of SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, or a fragment thereof; (ix) an antigenic fragment of SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, or SEQ ID NO: 97; (x) the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19, the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xi) a variant of the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the

amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xii) an antigenic fragment of the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xii) a combination of one or more of the sequences in (i)-(xii); (xiv) OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; (xv) a variant of OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; (xvi) an antigenic fragment of OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; (xvii) SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, or a fragment thereof; (xviii) a variant of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, or a fragment thereof; (xix) an antigenic fragment of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or SEQ ID NO: 9; (xx) SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof; (xxi) a variant of SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3,

SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof; (xxii) an antigenic fragment of SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, or SEQ ID NO: 8; (xxiii) the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; (xxiv) a variant of the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; (xxv) an antigenic fragment of the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; or (xxvi) a combination of one or more of the sequences in (xiv)-(xxv); with a test sample, under conditions that allow polypeptide/antibody complex to form; (b) detecting polypeptide/antibody complexes; wherein the detection of polypeptide/antibody complexes is an indication that antibodies specific for an *Anaplasma platys* polypeptide is present in the test sample. For example, and not to be limiting, the test sample can be a biological sample from a subject, and the detection of polypeptide/antibody complexes can be an indication that the subject has an *Anaplasma platys* infection or has been exposed to *Anaplasma platys*.

In one aspect, the methods of detecting antibodies that specifically bind an *Anaplasma platys* polypeptide described herein can further comprise determining the amount of antibody in the test sample. In yet a further aspect, the purified polypeptide can be attached to a substrate. In still a further aspect, the purified protein can be a fusion protein. For example, and not to be limiting, the purified polypeptide can be fused to an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, a heterologous protein, or a combination thereof. In a further aspect, the purified polypeptide can be in multimeric form.

In yet a further aspect, the methods of detecting antibodies that specifically bind an *Anaplasma platys* polypeptide described herein can further comprise a microtiter plate assay, reversible flow chromatographic binding assay, an enzyme linked immunosorbent assay, a radioimmunoassay,

a hemagglutination assay, a western blot assay, a fluorescence polarization immunoassay, or an indirect immunofluorescence assay.

Also described herein are methods of detecting an *Anaplasma platys* infection or exposure to *Anaplasma platys* in a subject comprising: (a) obtaining a biological sample from the subject; (b) contacting a purified polypeptide comprising the amino acid sequence of one or more of the following: (i) P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof (ii) a variant of P44 Box 1, P44, Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof (iii) an antigenic fragment of P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof (iv) SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, or a fragment thereof (v) a variant of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, or a fragment thereof (vi) an antigenic fragment of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, or SEQ ID NO: 45; (vii) SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, or a fragment thereof; (viii) a variant of SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, or a fragment thereof; (ix) an antigenic fragment of SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, or SEQ ID NO: 97; (x) the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the

amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xi) a variant of the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xii) an antigenic fragment of the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xiii) a combination of one or more of the sequences in (i)-(xii); (xiv) OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; (xv) a variant of OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; ((xvi) an antigenic fragment of OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; (xvii) SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID

NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, or a fragment thereof; (xviii) a variant of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, or a fragment thereof; (xix) an antigenic fragment of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or SEQ ID NO: 9; (xx) SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof; (xxi) a variant of SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof; (xxii) an antigenic fragment of SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, or SEQ ID NO: 8; (xxiii) the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; (xxiv) a variant of the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; (xxv) an antigenic fragment of the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; or (xxvi) a combination of one or more of the sequences in (xiv)-(xxv); with the biological sample under conditions that allow polypeptide/antibody complexes to form; and (c) detecting polypeptide/antibody complexes; wherein the detection of polypeptide/antibody complexes is an indication that the subject has an *Anaplasma platys* infection or exposure to *Anaplasma platys*. In one aspect, the methods of detecting an *Anaplasma platys* infection or exposure to *Anaplasma platys* in a subject can further comprise contacting the polypeptide/antibody complexes of step (b) with an indicator reagent that generates a measurable signal prior to the performance of step (c).

In a further aspect, the purified protein can be a fusion protein. For example, and not to be limiting, the purified polypeptide can be fused to an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, a heterologous protein, or a combination thereof. In yet a further aspect, the polypeptide/antibody

complexes can be detected at about 10 days after exposure or infection of the subject by *Anaplasma platys*.

Further described herein are methods of detecting *Anaplasma platys* polypeptides in a test sample comprising: (a) contacting one or more antibodies that specifically bind to a *Anaplasma platys* polypeptide with the test sample under conditions that allow polypeptide/antibody complexes to form; wherein the *Anaplasma platys* polypeptide comprises the amino acid sequence of one or more of the following: (i) P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof, (ii) a variant of P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof, (iii) an antigenic fragment of P44 Box 1, P44 Box 2, P44 Box 3, P44 Box 4, P44 Box 5, P44 Box 6, or a fragment thereof, (iv) SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, or a fragment thereof, (v) a variant of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, or a fragment thereof, (vi) an antigenic fragment of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, or SEQ ID NO: 45; (vii) SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, or a fragment thereof; (viii) a variant of SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, SEQ ID NO: 97, or a fragment thereof; (ix) an antigenic fragment of SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 40, SEQ ID NO: 93, SEQ ID NO: 41, SEQ ID NO: 94, SEQ ID NO: 42, SEQ ID NO: 95, SEQ ID NO: 43, SEQ ID NO: 96, SEQ ID NO: 44, or SEQ ID NO: 97; (x) the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid

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from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xi) a variant of the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xii) an antigenic fragment of the amino acid sequence comprising the amino acid from about position 20 to about position 40 of FIG. 23, the amino acid sequence comprising the amino acid from about position 40 to about position 64 of FIG. 23, the amino acid from about position 75 to about position 85 of FIG. 23, the amino acid sequence comprising the amino acid from about position 102 to about position 111 of FIG. 23, the amino acid from about position 170 to about position 190 of FIG. 23, the amino acid sequence comprising the amino acid from about position 178 to about position 222 of FIG. 23, the amino acid from about position 205 to about position 215 of FIG. 23, the amino acid sequence comprising the amino acid from about position 259 to about position 266 of FIG. 23, the amino acid from about position 270 to about position 290 of FIG. 23, the amino acid sequence comprising the amino acid from about position 319 to about position 340 of FIG. 23, the amino acid from about position 365 to about position 380 of FIG. 23, the amino acid sequence comprising the amino acid from about position 451 to about position 460 of FIG. 23, the amino acid from about position 1 to about position 41 of FIG. 19, the amino acid sequence comprising the amino acid from about position 78 to about position 85 of FIG. 19, the amino acid from about position 174 to about position 192 of FIG. 19, the amino acid sequence comprising the amino acid from about position 227 to about position 234 of FIG. 19 the amino acid from about position 276 to about position 294 of FIG. 19, the amino acid sequence comprising the amino acid from about position 416 to about position 433 of FIG. 19, or a fragment thereof; (xiii) a combination of one or more of the sequences in (i)-(xii); (xiv) OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; (xv) a variant of OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; ((xvi) an antigenic fragment of OMP-1X Box 1, OMP-1X Box 2, or a fragment thereof; (xvii) SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO:

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10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, or a fragment thereof; (xviii) a variant of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9, or a fragment thereof; (xix) an antigenic fragment of SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 10, SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or SEQ ID NO: 9; (xx) SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof; (xxi) a variant of SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, SEQ ID NO: 8, or a fragment thereof; (xxii) an antigenic fragment of SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 4, or SEQ ID NO: 8; (xxiii) the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; (xxiv) a variant of the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; (xxv) an antigenic fragment of the amino acid from about position 66 to about position 192 of FIG. 22, the amino acid from about position 70 to about position 180 of FIG. 22, a combination of the amino acid from about position 66 to about position 192 and the amino acid from about position 70 to about position 180 of FIG. 22, the amino acid from about position 240 to about position 312 of FIG. 22, the amino acid from about position 230 to about position 300 of FIG. 22, a combination of the amino acid from about position 240 to about position 312 and the amino acid from about position 230 to about position 300 of FIG. 22, or a fragment thereof; or (xxvi) a combination of one or more of the sequences in (xiv)-(xxv); (b) detecting polypeptide/antibody complexes; wherein the detection of polypeptide/antibody complexes is an indication that an *Anaplasma platys* polypeptide is present in the test sample. For example, and not to be limiting, the one or more antibodies can be monoclonal antibodies, polyclonal antibodies, Fab fragments, Fab' fragments, Fab'-SH fragments, F(ab')₂ fragments, Fv fragments, or single chain antibodies. In one aspect, the complexes of step (a) can be contacted with an indicator reagent prior to the performance of step (b).

In one aspect, the methods of detecting *Anaplasma platys* polypeptides in a test sample can further comprise determining the amount of *Anaplasma platys* polypeptides in the test sample. In yet a further aspect, the one or more antibodies can be attached to a substrate.

In a further aspect, the methods of detecting *Anaplasma platys* polypeptides in a test sample can further comprise a microtiter plate assay, reversible flow chromatographic

binding assay, an enzyme linked immunosorbent assay, a radioimmunoassay, a hemagglutination assay, a western blot assay, a fluorescence polarization immunoassay, or an indirect immunofluorescence assay.

The methods described herein can be used to detect antibodies or antibody fragments specific for *Anaplasma platys* polypeptides, *Anaplasma platys* polynucleotides, or a combination thereof in a test sample, such as a biological sample, an environmental sample, or a laboratory sample. A test sample can potentially comprise *Anaplasma platys* polynucleotides, *Anaplasma platys* polypeptides, or antibodies specific for *Anaplasma platys*. A biological sample can include, for example, sera, blood, cells, plasma, or tissue from a mammal such as a horse, cat, dog or human. The test sample can be untreated, precipitated, fractionated, separated, diluted, concentrated, or purified.

Disclosed herein are methods that comprise contacting an *Anaplasma platys* polypeptide with a test sample under conditions that allow a polypeptide/antibody complex, i.e., an immunocomplex, to form. That is, one or more of the polypeptides described herein specifically binds to an antibody specific for *Anaplasma platys* antigens located in the sample. One of skill in the art is familiar with assays and conditions that are used to detect antibody/polypeptide complex binding. The formation of a complex between polypeptides and anti-*Anaplasma platys* in the sample is detected. In one embodiment of the invention antibody-polypeptide complexes can be detected at about 10, 15, 20, 25, 30 or less days after exposure or infection of the subject by *Anaplasma platys*.

The antibodies described herein can be used in a method of the diagnosis of *Anaplasma platys* infection by obtaining a test sample from, e.g., a human or animal suspected of having an *Anaplasma platys* infection. Exposure to *Anaplasma platys* can also be detected. Exposure would include the presence of *Anaplasma platys* organisms without clinical symptoms and prior infection with *Anaplasma platys*. The test sample is contacted with antibodies of the invention under conditions enabling the formation of antibody-antigen complexes (i.e., immunocomplexes). The amount of antibody-antigen complexes can be determined by methodology known in the art. A level that is higher than that formed in a control sample indicates an *Anaplasma platys* infection. A control sample is a sample that does not comprise any *Anaplasma platys* polypeptides or antibodies specific for *Anaplasma platys*. In one embodiment of the invention an antibody is specific for *Anaplasma platys* P44 or *Anaplasma platys* OMP-1X antigens only. Alternatively, a polypeptide of the invention can be contacted with a test sample. *Anaplasma platys* antibodies in a positive body sample will form an antigen-antibody complex under suitable conditions. The amount of antibody-antigen complexes can be determined by methods known in the art.

Also disclosed herein are methods wherein the polypeptide/antibody complex is detected when an indicator reagent, such as an enzyme conjugate, which is bound to the antibody, catalyzes a detectable reaction. Optionally, an indicator reagent comprising a signal generating compound can be applied to the polypeptide/antibody complex under conditions that allow formation of a polypeptide/antibody/indicator complex. The polypeptide/antibody/indicator complex is detected. Optionally, the polypeptide or antibody can be labeled with an indicator reagent prior to the formation of a polypeptide/antibody complex. The method can optionally comprise a positive or negative control.

Disclosed herein are methods wherein one or more of the antibodies disclosed herein are attached to a solid phase or

substrate. A test sample potentially comprising a protein comprising one or more of the polypeptides described herein is added to the substrate. Antibodies that specifically bind to one or more of the polypeptides described herein are added. The antibodies can be the same antibodies used on the solid phase or can be from a different source or species and can be linked to an indicator reagent, such as an enzyme conjugate. Wash steps can be performed prior to each addition. A chromophore or enzyme substrate can be added and color is allowed to develop. The color reaction can be stopped and the color can be quantified using, for example, a spectrophotometer.

Also disclosed herein are methods wherein one or more of the antibodies described herein are attached to a solid phase or substrate. A test sample potentially comprising a protein comprising one or more of the polypeptides described herein is added to the substrate. Second anti-species antibodies that specifically bind one or more of the polypeptides described herein are added. These second antibodies can be from a different species than the solid phase antibodies. Third anti-species antibodies can also be added that specifically bind the second antibodies and that do not specifically bind the solid phase antibodies are added. The third antibodies can comprise an indicator reagent such as an enzyme conjugate. Wash steps can be performed prior to each addition. A chromophore or enzyme substrate is added and color is allowed to develop. The color reaction is stopped and the color can be quantified using, for example, a spectrophotometer.

Disclosed herein are methods of detecting antibodies that specifically bind an *Anaplasma platys* polypeptide or both. The method comprises contacting one or more of the purified polypeptides described herein with a test sample, under conditions that allow polypeptide/antibody complexes to form and detecting polypeptide/antibody complexes. The detection of polypeptide/antibody complexes is an indication that antibodies specific for *Anaplasma platys* are present in the test sample, and the absence of polypeptide/antibody complexes is an indication that antibodies specific for *Anaplasma platys* are not present in the test sample. The complexes can be contacted with an indicator reagent prior to the detection step. The amount of antibody in the test sample can be determined. The purified polypeptide can be attached to a substrate. The purified polypeptide can be a fusion protein wherein the purified polypeptide is fused to an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, a heterologous protein, or a combination thereof. The purified polypeptide can be in multimeric form. The method can comprise a microtiter plate assay, reversible flow chromatographic binding assay, an enzyme linked immunosorbent assay, a radioimmunoassay, a hemagglutination assay, a western blot assay, a fluorescence polarization immunoassay, or an indirect immunofluorescence assay.

Disclosed herein are methods of detecting an *Anaplasma platys* infection and/or exposure to *Anaplasma platys* in a subject. The method can comprise obtaining a biological sample from the subject; contacting a purified polypeptide of the invention with the biological sample under conditions that allow polypeptide/antibody complexes to form; and detecting polypeptide/antibody complexes. The detection of polypeptide/antibody complexes is an indication that the subject has an *Anaplasma platys* infection and/or exposure to *Anaplasma platys*. The absence of polypeptide/antibody complexes is an indication that the mammal has not had an *Anaplasma platys* infection and/or exposure to *Anaplasma*

platys. The polypeptide/antibody complexes can be contacted with an indicator reagent that generates a measurable signal prior to the performance of the detection step. The purified polypeptide can be a fusion protein wherein the purified polypeptide is fused to an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, a heterologous protein or a combination thereof. The polypeptide/antibody complexes can be detected at about 10 days after exposure or infection of subject by *Anaplasma platys*.

Also described herein are assays that include, but are not limited to those based on competition, direct reaction or sandwich-type assays, including, but not limited to enzyme linked immunosorbent assay (ELISA), western blot, IFA, radioimmunoassay (RIA), hemagglutination (HA), fluorescence polarization immunoassay (FPIA), and microtiter plate assays (any assay done in one or more wells of a microtiter plate). One assay comprises a reversible flow chromatographic binding assay. For example, described herein are assays similar to those described in U.S. Pat. No. 5,726,010.

Assays can use solid phases or substrates or can be performed by immunoprecipitation or any other methods that do not utilize solid phases. Where a solid phase or substrate is used, one or more of the polypeptides described herein can be directly or indirectly attached to a solid support or a substrate such as a microtiter well, magnetic bead, non-magnetic bead, column, matrix, membrane, fibrous mat composed of synthetic or natural fibers (e.g., glass or cellulose-based materials or thermoplastic polymers, such as, polyethylene, polypropylene, or polyester), sintered structure composed of particulate materials (e.g., glass or various thermoplastic polymers), or cast membrane film composed of nitrocellulose, nylon, polysulfone or the like (generally synthetic in nature). For example, the substrate can be sintered, fine particles of polyethylene, commonly known as porous polyethylene, for example, 10-15 micron porous polyethylene from Chromex Corporation (Albuquerque, N. Mex.). All substrate materials can be used in suitable shapes, such as films, sheets, or plates, or they can be coated onto or bonded or laminated to appropriate inert carriers, such as paper, glass, plastic films, or fabrics. Suitable methods for immobilizing peptides on solid phases include ionic, hydrophobic, covalent interactions and the like.

Disclosed herein is an assay format, wherein one or more polypeptides can be coated on a solid phase or substrate. A test sample suspected of containing an anti-*Anaplasma platys* antibody or fragment thereof is incubated with an indicator reagent comprising a signal generating compound conjugated to an antibody or antibody fragment specific for *Anaplasma platys* for a time and under conditions sufficient to form antigen/antibody complexes of either antibodies of the test sample to the polypeptides of the solid phase or the indicator reagent compound conjugated to an antibody specific for *Anaplasma platys* to the polypeptides of the solid phase. The reduction in binding of the indicator reagent conjugated to an anti-*Anaplasma platys* antibody to the solid phase can be quantitatively measured. A measurable reduction in the signal compared to the signal generated from a confirmed negative *Anaplasma platys* test sample indicates the presence of anti-*Anaplasma platys* antibody in the test sample. This type of assay can quantitate the amount of anti-*Anaplasma platys* antibodies in a test sample.

Disclosed herein is an assay format, wherein one or more of the polypeptides disclosed herein are coated onto a

support or substrate. One or more of the polypeptides disclosed herein can be conjugated to an indicator reagent and added to a test sample. This mixture can then be applied to the support or substrate. If *Anaplasma platys* antibodies are present in the test sample they will bind the polypeptide conjugated to an indicator reagent and to the polypeptide immobilized on the support. The polypeptide/antibody/indicator complex can then be detected. This type of assay can quantitate the amount of anti-*Anaplasma platys* antibodies in a test sample.

Disclosed herein is an assay format, wherein one or more polypeptides disclosed herein are coated onto a support or substrate. The test sample can be applied to the support or substrate and incubated. Unbound components from the sample can be washed away by washing the solid support with a wash solution. If *Anaplasma platys* specific antibodies are present in the test sample, they will bind to the polypeptide coated on the solid phase. This polypeptide/antibody complex can be detected using a second species-specific antibody that is conjugated to an indicator reagent. The polypeptide/antibody/anti-species antibody indicator complex can then be detected. This type of assay can quantitate the amount of anti-*Anaplasma platys* antibodies in a test sample.

The formation of a polypeptide/antibody complex or a polypeptide/antibody/indicator complex can be detected by radiometric, colorimetric, fluorometric, size-separation, or precipitation methods. Optionally, detection of a polypeptide/antibody complex is by the addition of a secondary antibody that is coupled to an indicator reagent comprising a signal generating compound. Indicator reagents comprising signal generating compounds (labels) associated with a polypeptide/antibody complex can be detected using the methods described above and include chromogenic agents, catalysts such as enzyme conjugates fluorescent compounds such as fluorescein and rhodamine, chemiluminescent compounds such as dioxetanes, acridiniums, phenanthridiniums, ruthenium, and luminol, radioactive elements, direct visual labels, as well as cofactors, inhibitors, magnetic particles, and the like. Examples of enzyme conjugates include alkaline phosphatase, horseradish peroxidase, beta-galactosidase, and the like. The selection of a particular label is not critical, but it will be capable of producing a signal either by itself or in conjunction with one or more additional substances.

Disclosed herein is an assay format wherein the *Anaplasma platys* polypeptides, polynucleotides, antibodies or combinations thereof can be used in conjunction with Raman spectroscopy. Raman spectroscopy is an analytical technique for chemical and biological analysis due to the wealth of information on molecular structures, surface processes, and interface reactions that can be extracted from experimental data. The Raman technique has been used with gene probe biosensors. U.S. Pat. No. 5,814,516 ('516 patent) discloses a gene probe biosensor comprising a support means, a SERS gene probe having at least one oligonucleotide strand having at least one SERS label, and a SERS active substrate disposed on the support means. The support means has at least one SERS gene probe adsorbed thereon. Biotargets such as bacterial and viral DNA, RNA and PNA are detected using a SERS gene probe via hybridization to oligonucleotide strands complementary to the SERS gene probe. U.S. Pat. No. 5,814,516 is hereby incorporated by reference in its entirety for its teaching of the Raman technique.

The '516 patent does not disclose or suggest operatively connecting a Raman gene probe with an integrated circuit

detection system to produce a biochip capable of SERS detection. U.S. Pat. No. 7,267,948 (948 patent) provides another assay format wherein the *Anaplasma platys* polypeptides, polynucleotides, antibodies or combinations thereof can be used. This '948 patent describes Raman and SERS assay methods and systems including microarrays, biosensors and biochips for the detection of biotargets such as DNA, proteins and pathogens using receptor probes. Receptor probes may include one or more bioreceptors selected from antibodies, DNA, enzymes, tissues, organelles, as well as other receptor probes, and combinations thereof described herein. U.S. Pat. No. 7,267,948 is hereby incorporated by reference in its entirety for its teaching of the Raman and SERS assay methods and systems.

Formation of the complex is indicative of the presence of anti-*Anaplasma platys* antibodies in a test sample. Therefore, the methods of the invention can be used to diagnose *Anaplasma platys* infection or exposure in a patient.

The methods described herein can also indicate the amount or quantity of anti-*Anaplasma platys* antibodies in a test sample. With many indicator reagents, such as enzyme conjugates, the amount of antibody present is proportional to the signal generated. Depending upon the type of test sample, it can be diluted with a suitable buffer reagent, concentrated, or contacted with a solid phase without any manipulation. For example, serum or plasma samples that previously have been diluted, or concentrate specimens such as urine, can be tested in order to determine the presence and/or amount of antibody present.

The polypeptides and assays described herein can be combined with other polypeptides or assays to detect the presence of *Anaplasma platys* along with other organisms. For example, polypeptides and assays of the invention can be combined with reagents that detect heartworm and/or *Borrelia burgdorferi* and/or *Anaplasma phagocytophilum* and/or *Ehrlichia canis*.

Also disclosed herein are methods of detecting an *Anaplasma* infection or exposure to *Anaplasma* in a subject. These methods can be used as an initial or final method to identify the presence of one or more species of *Anaplasma*. *Anaplasma* is a genus of rickettsiales bacteria. Anaplasmas can reside in host red blood cells and lead to the disease anaplasmosis.

Anaplasmas can require intermediate tick hosts for maturation, and flies may act as mechanical vectors. Species of *Anaplasma* include, but are not limited to, *Anaplasma marginate*, *Anaplasma centrale*, *Anaplasma mesaeterum*, *Anaplasma ovis*, and *Anaplasma platys*.

Disclosed herein are methods of detecting an *Anaplasma* infection or exposure to *Anaplasma* in a subject comprising: (a) obtaining a biological sample from the subject; (b) contacting a purified polypeptide encoded by one or more of the nucleotides of the following: SEQ ID NOs: 124-132 or a combination of one or more of the sequences of SEQ ID NOs: 124-132; with the biological sample under conditions that allow polypeptide complexes to form; and (c) detecting polypeptide complexes; wherein the detection of polypeptide complexes is an indication that the subject has an *Anaplasma* infection or exposure to *Anaplasma*. In addition, the methods can further comprise contacting the polypeptide complexes with an antibody that recognizes the polypeptide or polypeptide complex.

Also disclosed are methods of detecting the presence of *Anaplasma* in a sample by contacting said sample with a DNA probe or primer constructed to correspond to an

Anaplasma P44 nucleotide sequence, characterized in that the probe or primer comprises one or more of the nucleotides of SEQ ID NOs: 124-132.

Also disclosed are methods of detecting the presence of *Anaplasma* in a sample by contacting said sample with a DNA probe or primer constructed to correspond to an *Anaplasma* P44 nucleotide sequence, characterized in that the probe or primer comprises one or more nucleotides capable of hybridizing to one or more of the nucleotides of SEQ ID NOs: 124-132.

A method for detecting *Anaplasma* in a sample obtained from a subject, comprising (a) providing a primer set comprising: (i) one or more forward primers capable of hybridizing to or amplifying: one or more of the nucleotides of SEQ ID NOs: 124-132 and (ii) one or more forward primers capable of hybridizing to or amplifying: one or more of the nucleotides of SEQ ID NOs: 124-132; (b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and (c) determining the length or sequence of the PCR products of step (b), wherein the presence of a PCR product having a length or sequence which corresponds to the length or sequence, respectively, of that region of the *Anaplasma* nucleotide sequence which is located between the regions to which the one or more forward primers and the one or more reverse primers bind is indicative of the presence of *Anaplasma* in the sample.

Also disclosed herein are isolated or purified polynucleotides comprising the sequence of one or more of the polynucleotide sequences of SEQ ID NOs: 124-132, or a fragment thereof. Also disclosed herein are isolated or purified polynucleotides comprising 80%, 85%, 90%, 95%, or 100% sequence identity to the sequence of one or more of the polynucleotide sequences of SEQ ID NOs: 124-132, or a fragment thereof.

Also disclosed are vectors for transformation of a host cell, said vector comprising the sequence of one or more of the polynucleotide sequences of SEQ ID NOs: 124-132, or a fragment thereof.

Also disclosed herein are isolated or purified polypeptides encoded by a polynucleotide sequences wherein the polynucleotide sequence comprises the sequence of one or more of the polynucleotide sequences of SEQ ID NOs: 124-132, or a fragment thereof. Also disclosed herein are isolated or purified polypeptides encoded by a polynucleotide sequences wherein the polynucleotide sequence comprises 80%, 85%, 90%, 95%, or 100% sequence identity to the sequence of one or more of the polynucleotide sequences of SEQ ID NOs: 124-132, or a fragment thereof.

EXAMPLES

Example 1

Materials and Methods

A. platys-Infected Dogs.

Dogs that were naturally infected with *A. platys* were identified in Lara, Venezuela, in 2007 by observation of bacterial inclusions (morulae) in platelets from blood smears, and cases were confirmed by PCR and sequencing using primer pairs specific for *A. platys* 16S rRNA (EP1-EP3 and EP2-EP3).²⁹ Naturally infected dogs in Taichung, Taiwan and the Democratic Republic of Congo were identified and confirmed by PCR using primer pair EPLATS-EPLAT.⁴²

Cloning of p44 Expression Locus from *A. platys*.

DNA samples from three dogs from Venezuela and one dog from Taiwan were used as templates. By aligning the

p44/msp2 expression loci from *A. phagocytophilum* and *A. marginate*, several degenerate primers were designed for conserved regions of the locus (FIG. 1, Table 1). Using the first and the second primer pairs F1-R1 and F1-R2, (hemi-nested touchdown PCR⁵² was used to amplify the tr1 and omp-1X gene sequences from *A. platys*. In order to avoid truncating p44 pseudogenes in the *A. platys* genome, primer F3 was designed to be upstream of the predicted p44 open reading frame. p44ES sequences were amplified by nested touchdown PCR using primer pairs F2-R3 and F3-R4. Amplification was performed as previously described.⁶⁸ The amplified DNA fragments were cloned using the TA cloning kit (Invitrogen, Carlsbad, Calif.) and sequenced with M13 forward or M13 reverse sequencing primers. All sequencing data were assembled using the SeqMan program (DNASTAR Inc., Madison, Wis.). To confirm the assembly the entire locus was amplified using primers F1 and R5 (Table 1).

Phylogenetic Analysis.

The deduced amino acid sequences for Tr1, OMP-1/OMP-1X, and P44ES from *A. marginate*, *A. phagocytophilum*, and *A. platys* were aligned using the MegAlign program (DNASTAR Inc.) by the Clustal W method.

Protein Structure Analysis Using Bioinformatics Tools.

SignalP 3.0 server trained on Gram-negative bacteria (<http://www.cbs.dtu.dk/services/SignalP/>) was used for signal peptide sequence analysis. The secondary structures of P44 and OMP-1X were predicted by PRED-TMBB⁴ and hydrophobicity analysis and the hydrophobic moment profile method, as previously described.^{30, 35} The antigenic index and surface probability were determined using the Protean program (DNASTAR Inc.).

ELISA Analysis of OMP-1X-Specific Peptide.

The OMP-1X peptide from *A. platys* was synthesized at Biomatik (Wilmington, Del.). The purity of the peptide was greater than 98%, as assessed by high-performance liquid chromatography. The wells of a 96-well microtiter plate were coated with 200 ng peptide/well and the ELISA was performed as previously described.⁶⁰ Samples were from three dogs that were PCR-positive for *A. platys* (TW 431, TW 270, and TW 210), and three dogs that were both PCR-negative for *A. platys* and antigen dot blot—negative for *A. phagocytophilum* (E05-290, E10-0062, and E10-0075). In addition, horse anti-*A. phagocytophilum* positive sera (EQ002, EQ006, and E09-0011)^{65, 71} were used to confirm the absence of OMP-1X peptide antigen cross-reactivity with anti-*A. phagocytophilum* antibodies. The horseradish peroxidase substrate 2,2'-azido-di-(3-ethyl)-benzthiazoline-6-sulfonic acid (Sigma, St. Louis, Mo.) in 70 mM citrate buffer (pH 4.2) applied, and absorbance values at 415 and 492 nm were measured in an ELISA plate reader (Molecular Devices, Sunnyvale, Calif.) as previously described.⁶⁸ Results were presented as optical density at 415 nm minus that at 492 nm ($OD_{415}-OD_{492}$), and the cutoff for a positive reaction was set at greater than the mean $OD_{415}-OD_{492}+3$ SD for the negative control samples ($OD>0.165$). The assay was repeated at least three times.

Nucleotide Sequence Accession Number.

The *A. platys* tr1-omp-1X-p44ES sequences from two naturally infected dogs from Venezuela were assembled and deposited at GenBank under accession numbers GQ868750 and GU357491. Additional p44ES and p44 sequences were deposited at GenBank under accession numbers GU357492, GU357493, GU357494, GU357495, GU357496, GU357497, and HQ738571.

Results

A. platys tr1-omp1-p44ES cluster sequencing and assembly. Three degenerate primers and one primer at a highly conserved region of tr1 upstream region were designed based on conserved regions of the aligned tr1-omp1X-omp1N-p44 cluster of *A. phagocytophilum* and YP_154239 (hypothetical protein AM1138; transcriptional regulator)-YP_154240 (outer membrane protein 1; outer membrane protein 4)-YP_154241 (msp2 operon associated gene 3; outer membrane protein 3)-YP_154243 (msp2 operon associated gene 2)-YP_154244 (msp2 operon associated gene 1)-YP_154245 (msp2) cluster of *A. marginate* (FIG. 1, Table 1). The first touchdown PCR was designed to amplify the entire fragment using primers F1 and R1. The PCR products from the two dog DNA specimens were then used as templates for hemi-nested touchdown PCRs using primers F1 and R2 (FIG. 1, Table 1). As a result, a single band of about 2,100 bp was amplified (fragment A). The PCR products were TA cloned and sequenced. The sequence results showed this fragment contained *A. platys* tr1 and omp-1X. The downstream region of fragment A was amplified by nested touchdown PCR, using the PCR products obtained with primers F1 and R1 as templates, with primer F2 designed based on the fragment A sequence and primer R3 designed based on p44 (msp2) sequences conserved between *A. phagocytophilum* and *A. marginate*. As a result, a single band of approximately 1,100 bp was amplified (fragment B). The PCR products were TA cloned and sequenced. The sequence results showed that this fragment contained a partial *A. platys* p44 sequence. To amplify *A. platys* full-length p44, primer F3 was designed based on fragment B sequence and primer R4 was designed based on the conserved region of valS found downstream of p44 (msp2) in both *A. phagocytophilum* and *A. marginate*. Further touchdown PCR was done using primers F1 and R4. The PCR products were then used as templates for hemi-nested touchdown PCRs using primers F3 and R4. As a result, a single band of about 1,700 bp was amplified (fragment C). The PCR products were TA cloned and sequenced. The sequence results showed this fragment contained full length *A. platys* p44 sequences. The final assembled sequences 3,957 bp from dogs 1 and 2, respectively contained the entire *A. platys* p44ES locus, and the G+C content was 47.46–47.51%.

The final assembled sequence of 3957 bp from Venezuelan dogs 1 and 2 contained the entire *A. platys* p44ES locus. The sequence average coverage of the entire locus was 8.3 fold (5 to 15 fold). To confirm the assembly was from a complete genomic locus, primer R5 was designed to be downstream of the predicted p44 open reading frame and one more touchdown PCR was conducted using primers F1 and R5. A single band, approximately 3.9 kb was amplified (fragment D), indicating the fragment containing the entire locus was amplified from the blood of dog 2 (FIG. 1C). The G+C content was determined to be 47.46% to 47.51%. The synteny among the entire outer membrane protein gene clusters of *A. platys* and the two previously sequenced *Anaplasma* species was analyzed using the Artemis Comparison Tool.¹⁴ The tr1 sequences were conserved among the three *Anaplasma* species (FIG. 2). The 5' and 3' regions of p44ES were conserved between *A. platys* and *A. phagocytophilum*, but not between *A. platys* and *A. marginate* (FIG. 2).

A. platys Tr1 Structure.

Three similar (97.8% to 99.5%) *A. platys* tr1 sequences were obtained from two dogs from Venezuela and one dog from Taiwan. The predicted molecular mass of *A. platys* Tr1 was 21.0 to 21.1 kDa with an isoelectric point of 5.50 to 5.80

(Table 2). Tr1 was not predicted to have a signal peptide, thus was a cytoplasmic protein, as analyzed by SignalP 3.0. Tr1 was predicted to contain a putative N-terminal helix-turn-helix DNA-binding domain based on the analysis of the NCBI conserved domain database, suggesting that it was a transcriptional regulator. The amino acid sequence identity between *A. platys* Tr1 and *A. phagocytophilum* Tr1 (YP_505749) was 84.8% to 86.4%, and that between *A. platys* Tr1 and *A. marginate* Tr (YP_154239) was 73.1% to 74.1%.

A. platys OMP-1X structure. Three nearly identical (99.1%) *A. platys* omp-1X sequences were obtained from two dogs from Venezuela and one dog from Taiwan. Using SignalP 3.0 server, OMP-1X was predicted to have a signal peptide with a cleavage site between positions 23 and 24. The predicted molecular mass of mature *A. platys* OMP-1X was 31.9 kDa with an isoelectric point of 7.27 to 7.92 (Table 2). The secondary structure of OMP-1X was then examined, using PRED-TMBB.⁴ The discrimination value of the OMP-1X amino acid sequence was 2.907, which is below the threshold value of 2.965, making OMP-1X likely to be a β -barrel protein localized to the outer membrane. Hydrophobicity analysis and the hydrophobic moment profile program developed for the porin structure prediction,³⁵ predicted 14 β -strands in OMP-1X. The protein sequences most closely related to *A. platys* OMP-1X were *A. phagocytophilum* OMP-1X (YP_505750; 45.9%-46.3% identity) and *A. marginate* OMP-1 (YP_154240; 39.8% identity). A phylogenetic analysis showed that OMP-1X homologs in *Anaplasma* spp. formed a cluster that was distinct from the cluster of most closely related OMP-1X homologs in each *Ehrlichia* spp. (FIG. 3).

A. platys P44ES Structure.

Four P44ES sequences (GQ868750, GU357491, GU357492, and GU357493) were obtained from three dogs from Venezuela. Using SignalP 3.0 sever P44ES was predicted to have a putative signal peptide with a cleavage site between positions 21 and 22. The molecular mass of the mature P44ES protein was predicted to be 41.2 to 41.4 kDa with an isoelectric point of 5.30 to 5.72 (Table 2). By PRED-TMBB⁴ analysis, the discrimination value of the P44 amino acid sequence was 2.920 which was below the

threshold value of 2.965, making P44 likely to be a β -barrel protein localized to the outer membrane. Hydrophobicity analysis and the hydrophobic moment profile predicted 16 β -strands in P44. Alignment of total nine *A. platys* P44 sequences (the four P44 full-length proteins from dogs 1, 2, and 3, and the five partial P44 sequences obtained from dogs 1, 2 and Taiwan) using HVF and HVR primers, revealed a single central hypervariable region (aa position 193-247) of approximately 55 amino acid residues, and N-terminal and C-terminal conserved regions of approximately 192 and 159 amino acid residues, respectively. The conserved amino acids C, C, W, and A from the P44 hypervariable region of *A. phagocytophilum* P44⁴¹ were also detected in the hypervariable region of *A. platys* P44. The C terminus of *A. platys* P44 ends with phenylalanine, as does the C terminus of *A. phagocytophilum* P44.³⁰ The amino acid sequence identity between *A. platys* P44ES and *A. phagocytophilum* P44-18ES (YP_505752) was 55.0% to 56.9%, and that between *A. platys* P44ES and *A. marginate* Msp2 (YP_154245) was 41.5% to 42.1%. Phylogenetic analysis placed full-length *A. platys* p44s between *A. phagocytophilum* p44s and *A. marginate* msp2s (FIG. 4). The sequence identities of the conserved N-terminal 192 amino acids and the conserved C-terminal 159 amino acids of *A. platys* and *A. phagocytophilum* P44s were 57.3% and 66.7%, respectively.

Primer pairs (HVF and HVR, Table 1) designed based on *A. platys* p44 conserved region amplified only *A. platys* DNA, but not *A. phagocytophilum* and *A. marginate* DNA. Alignment of a total of nine *A. platys* P44 hypervariable regions and flanking conserved regions with P44/Msp2 sequences among *A. phagocytophilum* P44s and *A. marginate* Msp2s revealed several *A. platys*-specific sequences: TGTAAGSDVDYVSKF (SEQ ID NO: 92; aa position 23-37), TRVEWKAE (SEQ ID NO: 93; aa position 78-85), AAIEVKFAEAVGTSK (SEQ ID NO: 94; aa position 174-189), SWKCTQTG (SEQ ID NO: 95; aa position 207-214), AAKAEDLS (SEQ ID NO: 96; aa position 248-255) and ATTNKTKEF (SEQ ID NO: 97; aa position 378-386). These *A. platys*-specific p44 regions were utilized as serologic test antigens to distinguish from *A. phagocytophilum* or *A. marginate* infections.

TABLE 1

Primers used for PCR amplification of <i>A. platys</i> P44ES cluster		
Primer	Sequence	Note
F1	5'-ATTATGTATGATTATCCTAAGTTATCTGAG-3' (SEQ ID NO: 82)	tr 1/tr highly conserved upstream region
F2	5'-GGGATATCGGCGTTGATAGGG-3' (SEQ ID NO: 83)	<i>A. platys</i> omp-1X downstream genomic walking
F3	5'-GGTTTGTGTTGCTGGTGATTGGAGG-3' (SEQ ID NO: 84)	<i>A. platys</i> p44 upstream genomic walking
R1	5'-GCAACCTAACACCMAYTCMCCACC-3' (SEQ ID NO: 85)	p44ES/Msp2 C-terminal highly conserved region
R2	5'-TATACTAAAAAAGAAATTAAGTCAAGAG-3' (SEQ ID NO: 86)	Conserved intergenetic region between omp-1X/omp1 and omp-1N/opag3
R3	5'-ATGGTAGAAAACCCAGCAAA-3' (SEQ ID NO: 87)	p44ES/Msp2 N-terminal conserved region
R4	5'-CACGTNTTTAGTTACTGCCA-3' (SEQ ID NO: 88)	p44ES/Msp2ES from downstream conserved valS gene

TABLE 1-continued

Primers used for PCR amplification of <i>A. platys</i> P44ES cluster		
Primer	Sequence	Note
R5	5'-GTACTAGTCAGCGCCACTAACATCAA-3' (SEQ ID NO: 89)	p44ES/Msp2ES downstream region for complete locus confirmation
HVF	5'-GAAGAATACGAAAGCGGCGG-3' (SEQ ID NO: 90)	<i>A. platys</i> P44 hypervariable cloning region
HVR	5'-TACTTAGGTCTTCCGCTTTCGC-3' (SEQ ID NO: 91)	<i>A. platys</i> P44 hypervariable cloning region

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ELISA Analysis of OMP-1X.

When the Clustal W method was used to compare *A. platys* OMP-1X to its phylogenetically closest OMP-1 homologs—*A. phagocytophilum* OMP-1X (YP_505750), *A. marginate* OMP1 (YP_154240), *E. canis* P30-19 (AAK28680), *E. ruminantium* Map1-related protein (YP_180721), *E. ewingii* OMP-1-1 (AB036240), and *E. chaffeensis* OMP-1M (YP_507903), we identified a unique region in the *A. platys* OMP-1X amino acid sequence. This sequence, AVQEKKPPEA (SEQ ID NO: 98), is within the 2nd external loop from the N-terminus based on the hydrophobicity analysis and the hydrophobic moment profile program. The sequence is predicted to be highly antigenic and surface exposed by Protean program may aid in differential serodiagnosis (FIG. 14). The *A. platys* OMP-1X peptide was synthesized and its reactivity to known infected dog sera was tested by ELISA. Three *A. platys* PCR-positive dog sera reacted with the synthesized OMP-1X peptide antigen. Sera from *A. platys* PCR-negative dogs and horse anti-*A. phagocytophilum* serum did not react with the OMP-1X peptide antigen (FIG. 15), suggesting that this antigen can be used for species-specific serodiagnosis of *A. platys*.

locus of *A. platys* is also the site of active recombination, and multiple p44 donor sequences also exist in the *A. platys* genome.

The synteny analysis suggested that the major outer membrane expression locus existed in a common ancestor of the three *Anaplasma* species in existence today. Furthermore, the locus appears to have diverged primarily by duplicating omp-1-like sequences between tr1 and p44/msp2ES; *A. marginate*, *A. phagocytophilum*, and *A. platys* have 4, 2, and 1 omp-1-like sequences, respectively.

Three species of *Anaplasma* infect different host cells, namely neutrophils, erythrocytes, and platelets. The comparative study of between *A. phagocytophilum*, *A. marginate*, and *A. platys* P44/Msp2s, and OMP-1 homologs provided a new window of opportunity to investigate different *Anaplasma* host cell tropism.

Tr1, a putative transcription factor, is more highly expressed in tick cells infected with *A. phagocytophilum* than in human leukemic HL-60 cells infected with *A. phagocytophilum*, which suggested that Tr1 may regulate genes involved in the bacterial infection cycle in ticks.^{44, 64}

TABLE 2

Properties of <i>A. platys</i> p44ES cluster								
Protein	Upstream intergenic space (bp)	Gene Length (bp)	Protein Size (amino acids) ^a	Signal peptide (amino acids) ^b	Molecular mass ^a (Da)	Isoelectric point	Protein	Upstream intergenic space (bp)
Tr1	NA ^c	558	185	NA	21010.6-20952.6 ^d	5.50-5.80 ^d	Tr1	NA ^c
OMP-1X	306	933	301	23	31885.0-31942.1 ^d	7.27-7.92 ^d	OMP-1X	306
P44ES	682	1221	380-386 ^d	21	41167.3-41359.5 ^d	5.30-5.72 ^d	P44ES	682

^aMature protein.^bPredicted cleavage site.^cNot applicable.^dRange among strains.

Discussion

In the present study, the entire 4 kb *A. platys* p44ES locus, containing tr1, omp-1X and p44 genes, was sequenced, providing new insight into the p44 expression locus and the major surface antigen of *A. platys*. From each infected dog different p44ES sequences were detected, showing mixed P44 allele population of *A. platys* is present in the dog blood in a given time point similar to *A. phagocytophilum* p44 expression in humans and horses^{38, 39, 65} or *A. marginate* msp2 in the blood of cattle.^{18, 21, 47} In addition three more different hypervariable regions were detected in partial *A. platys* p44 gene sequences, suggesting the p44-expression

55 In contrast, Tr is expressed similarly in bovine red blood cells and IDE8 tick cell cultures infected with *A. marginale*.⁵

In *A. phagocytophilum* tr1, two omp-1s and p44E were co-expressed.³⁹ In the cattle blood, the aforementioned and related genes were co-expressed with the exception of the third msp2-associated genes.⁴⁸ Omp-1s are major surface antigens of *Ehrlichia* species, also has a role in *A. platys* infection cycle. OMP-1 homologous proteins are major surface antigens in *Ehrlichia* species,^{23, 46, 57, 62, 66} and OMP-1X functions similarly in the *A. platys* infection cycle. *A. platys* OMP-1X is predicted to have a β -barrel structure similar to that of *E. chaffeensis* P28 and OMP-1F,³⁷ and is thus a porin.

The fact that *A. phagocytophilum* and *A. marginate* P44/Msp2 transcripts were distinct between mammals and ticks advocates multiple physiological adaptations between different host environments.^{44, 53, 71} Furthermore, *A. phagocytophilum* p44 gene conversion in mammalian hosts suggested its role in antigenic variation.^{8, 19, 38, 65} In cattle, *A. marginate* MSP2s allows antigenic variation for persistent infection.^{6, 11, 47} *A. platys* P44, therefore, plays an important role in determining persistent or cyclical rickettsemia.

It is not known whether *A. platys* p44ES undergoes nonsegmental gene conversion (as in *A. phagocytophilum* to generate identical P44s from a large number of donor loci) or segmental gene conversion (as in *A. marginate* to generate mosaic Msp2ES from a small number of donor loci).^{39, 47} P44 has a role in the interaction between *A. phagocytophilum* and host cells.^{36, 49, 64} The P44 of *A. phagocytophilum* is the major surface antigen useful for serologic diagnosis of human granulocytic anaplasmosis, and has a role in the interaction between *A. phagocytophilum* and host cells. P44s also elicits a porin activity for passive diffusion of hydrophilic solutes.

Based on the present study, recombinant or peptide-based OMP-1X and P44 antigen can be prepared for testing the applicability of *A. platys* serodiagnosis. P44 can also serve as a specific and sensitive target for PCR diagnosis for human granulocytic anaplasmosis, and thus can be tested for *A. platys* infection or exposure.

A. phagocytophilum is known to infect dogs in regions where the *Ixodes* tick is endemic.^{2, 24, 50, 51} *A. platys* inclusions in the platelets of a naturally infected dog cross-reacted with mouse anti-*A. phagocytophilum* serum.³² It was important, therefore, to develop a method for distinguishing *A. platys* infection from *A. phagocytophilum* infection. Since the p44 primer pair: HVF and HVR described herein, is specific to *A. platys*, it was expected to be useful for species-specific PCR diagnosis. P44 of *A. phagocytophilum* is the major surface antigen used for serologic diagnosis of human granulocytic anaplasmosis.^{1, 16, 27, 31, 70} In the present study, several *A. platys*-specific amino acid sequences were identified within P44 proteins that can be used as serologic test antigens to provide differential diagnosis from other *Anaplasma* species infection. Additionally, *Ehrlichia* OMP-1/P28/P30/MAP families are immunodominant major outer membrane proteins useful for serodiagnosis.^{45, 62, 63, 68} The alignment results showed a distinct fragment (~20 amino acids) in *A. platys* Omp-1X that was not observed in the closest homologs from *Anaplasma* and *Ehrlichia* spp. Furthermore, this region was identical in *A. platys* samples from the geographically separated regions of Venezuela and Taiwan. This specific OMP-1X peptide antigen did not cross-react with anti-*A. phagocytophilum* serum, and therefore can be suitable for species-specific differential serodiagnosis of *A. platys*.

Since the only available source of *A. platys* DNA was a small amount of DNA purified from infected dog blood specimens, touchdown PCR was employed to amplify the available canine DNA. Incorrect base pairings resulting from amplification were minimized by using a high-fidelity Taq polymerase

Example 2

A. platys Expression Locus Analysis.

DNA specimens from three dogs naturally infected with *A. platys* at Lara, Venezuela in 2007 were used as the template for the amplification and sequencing process. *A. platys* infection of the dog was confirmed by PCR and

sequencing of the 16S rRNA of *A. platys* as well as by observation of bacterial inclusions (morulae) in platelets in the blood smear. By aligning *A. phagocytophilum* and *A. marginate* p44/msp2 expression loci, several degenerate primers were designed based upon conserved regions (FIG. 1, Table 1). Using the first primer pair F1 and R1, and the second primer pair F1 and R2, (hemi-) nested touchdown PCR amplified the *A. platys* tr1 and omp-1X sequences. In order to avoid truncated p44 pseudogenes in *A. platys* genome, primer F3 for the 5' upstream of the predicted p44 ORF was designed. p44ES sequences were amplified by nested touchdown PCR with primer pairs F2 and R3, and F3 and R4. Amplification was performed as previously described. The amplified DNA fragments were cloned using a TA cloning kit (Invitrogen, Carlsbad, Calif.) and sequenced with M13 Forward or M13 Reverse sequencing primers. All sequencing data was assembled using SeqMan program of DNASTAR software (DNASTAR Inc., Madison, Wis.). The deduced amino acid sequences of *A. marginate*, *A. phagocytophilum*, and *A. platys* tr1, Omp-1X and p44ES were aligned using the MegAlign program of DNASTAR software by the Clustal W method.

P44 Secondary Structure Prediction.

The P44 secondary structure was predicted by hydrophobicity and the hydrophobic moment profile method as previously described. Antigenic Index and surface probability were examined by Protean program of DNASTAR.

All patents, patent applications, and other scientific or technical writings referred to anywhere herein are incorporated by reference in their entirety. The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" can be replaced with either of the other two terms, while retaining their ordinary meanings. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by embodiments, optional features, modification and variation of the concepts herein disclosed can be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Throughout this application, various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this pertains. The references disclosed are also individually and specifically incorporated by reference herein for the material contained in them that is discussed in the sentence in which the reference is relied upon.

Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication

provided herein may be different from the actual publication dates, which can require independent confirmation.

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His Glu Gly Ala Ser Gly Phe Phe Ala Ser Val Gln Tyr Lys Tyr Gly
          35             40             45

Ala Pro Tyr Phe Gly Ser Leu Thr Leu Glu Ser Gly Gly Lys Thr Leu
          50             55             60

Asn Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala
          65             70             75             80

Ala Asp Glu Ala Ala Glu Pro Ala Thr Pro Ala Pro Ser Ser Pro Glu
          85             90             95

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Gly Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Thr
 100 105 110
 Tyr Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Ile
 115 120 125
 Gly Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val
 130 135 140
 Asn Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala
 145 150 155 160
 Ala Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Ala
 165 170 175
 Gln Lys Tyr Phe Val Thr Leu Glu Asn Arg Asp Val Ala Ile Thr Ser
 180 185 190
 Leu Val Ala Asn Ala Cys Tyr Asp Met Met Pro Ala Thr Ser Ser Ile
 195 200 205
 Ala Pro Ser Ala Cys Val Gly Val Gly Val Ser Phe Ala Lys Leu Leu
 210 215 220
 Gly Val Leu Glu Gln Arg Leu Thr Tyr Gln Phe Lys Gly Gly Leu Gln
 225 230 235 240
 Tyr Phe Val Gly Lys Lys Thr Val Ile Phe Leu Ser Gly Tyr Val Ser
 245 250 255
 Thr Ile Gly Gly Arg Lys Ile Thr Gln Val Lys Val Lys His Arg Leu
 260 265 270
 Ser Thr Pro Gln Thr Ala Ser Val Gly Ala Glu Gly Ser Gly Ala Gly
 275 280 285
 Ala Ala Ala Thr Ser Ser Ala Pro Pro Ala Pro Ile His Leu Leu Tyr
 290 295 300
 Pro Asp Ala Asn Leu Ser Leu Ala Tyr Tyr Gly Phe Glu Leu Gly Val
 305 310 315 320
 Arg Leu Val Phe

<210> SEQ ID NO 2
 <211> LENGTH: 117
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 2

Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala Ala
 1 5 10 15
 Asp Glu Ala Ala Glu Pro Ala Thr Pro Ala Pro Ser Ser Pro Glu Gly
 20 25 30
 Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Thr Tyr
 35 40 45
 Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Thr Gly
 50 55 60
 Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val Asn
 65 70 75 80
 Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala Ala
 85 90 95
 Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Ala Gln
 100 105 110
 Lys Tyr Phe Val Thr
 115

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<210> SEQ ID NO 3
<211> LENGTH: 68
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 3

Leu Thr Tyr Gln Phe Lys Gly Gly Leu Gln Tyr Phe Val Gly Lys Lys
1           5           10           15

Thr Val Ile Phe Leu Ser Gly Tyr Val Ser Thr Ile Gly Gly Arg Lys
                20           25           30

Ile Thr Gln Val Lys Val Lys His Arg Leu Ser Thr Pro Gln Thr Ala
            35           40           45

Ser Val Gly Ala Glu Gly Ser Gly Ala Gly Ala Ala Ala Thr Ser Ser
50           55           60

Ala Pro Pro Ala
65

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<210> SEQ ID NO 4
<211> LENGTH: 185
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 4

Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala Ala
1           5           10           15

Asp Glu Ala Ala Glu Pro Ala Thr Pro Ala Pro Ser Ser Pro Glu Gly
20           25           30

Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Thr Tyr
35           40           45

Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Thr Gly
50           55           60

Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val Asn
65           70           75           80

Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala Ala
85           90           95

Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Ala Gln
100          105          110

Lys Tyr Phe Val Thr Leu Thr Tyr Gln Phe Lys Gly Gly Leu Gln Tyr
115          120          125

Phe Val Gly Lys Lys Thr Val Ile Phe Leu Ser Gly Tyr Val Ser Thr
130          135          140

Ile Gly Gly Arg Lys Ile Thr Gln Val Lys Val Lys His Arg Leu Ser
145          150          155          160

Thr Pro Gln Thr Ala Ser Val Gly Ala Glu Gly Ser Gly Ala Gly Ala
165          170          175

Ala Ala Thr Ser Ser Ala Pro Pro Ala
180          185

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<210> SEQ ID NO 5
<211> LENGTH: 324
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 5

Met Lys Lys Arg Ile Arg Val Phe Ala Phe Ala Val Phe Met Leu Gly
 1 5 10 15
 Leu Pro Ser Val Ser Phe Ala Ser Pro Gln Pro Val Asp Phe Ser Tyr
 20 25 30
 His Glu Gly Ala Ser Gly Phe Phe Ala Ser Val Gln Tyr Lys Tyr Gly
 35 40 45
 Ala Pro Tyr Phe Gly Ser Leu Thr Leu Glu Ser Gly Gly Lys Ile Leu
 50 55 60
 Asn Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala
 65 70 75 80
 Ala Asp Glu Ala Ala Gly Pro Ala Thr His Ala Pro Ser Ser Pro Glu
 85 90 95
 Gly Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Thr
 100 105 110
 Tyr Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Ile
 115 120 125
 Gly Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val
 130 135 140
 Asn Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala
 145 150 155 160
 Ala Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Thr
 165 170 175
 Gln Lys Tyr Phe Val Thr Leu Glu Asn Arg Asp Val Ala Ile Thr Ser
 180 185 190
 Leu Val Ala Ser Ala Cys Tyr Asp Met Met Pro Ala Thr Ser Ser Ile
 195 200 205
 Ala Pro Ser Ala Cys Val Gly Val Gly Val Ser Phe Ala Lys Leu Leu
 210 215 220
 Gly Val Leu Glu Gln Arg Leu Thr Tyr Gln Phe Lys Gly Gly Leu Gln
 225 230 235 240
 Tyr Phe Val Gly Lys Lys Thr Val Ile Phe Leu Ser Gly Tyr Val Ser
 245 250 255
 Thr Ile Gly Gly Arg Lys Ile Ser Gln Val Lys Val Lys His Arg Leu
 260 265 270
 Pro Thr Pro Gln Thr Ala Ser Val Gly Ala Glu Gly Ser Gly Ser Gly
 275 280 285
 Ala Ala Ala Thr Ser Ser Ala Pro Pro Ala Leu Ile His Leu Leu Tyr
 290 295 300
 Pro Asp Ala Asn Leu Ser Leu Ala Tyr Tyr Gly Phe Glu Leu Gly Val
 305 310 315 320
 Arg Leu Val Phe

<210> SEQ ID NO 6

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 6

Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala Ala
 1 5 10 15
 Asp Glu Ala Ala Gly Pro Ala Thr His Ala Pro Ser Ser Pro Glu Gly
 20 25 30

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Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Thr Tyr
 35 40 45

Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Thr Gly
 50 55 60

Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val Asn
 65 70 75 80

Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala Ala
 85 90 95

Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Thr Gln
 100 105 110

Lys Tyr Phe Val Thr
 115

<210> SEQ ID NO 7
 <211> LENGTH: 68
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 7

Leu Thr Tyr Gln Phe Lys Gly Gly Leu Gln Tyr Phe Val Gly Lys Lys
 1 5 10 15

Thr Val Ile Phe Leu Ser Gly Tyr Val Ser Thr Ile Gly Gly Arg Lys
 20 25 30

Ile Ser Gln Val Lys Val Lys His Arg Leu Pro Thr Pro Gln Thr Ala
 35 40 45

Ser Val Gly Ala Glu Gly Ser Gly Ser Gly Ala Ala Ala Thr Ser Ser
 50 55 60

Ala Pro Pro Ala
 65

<210> SEQ ID NO 8
 <211> LENGTH: 185
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 8

Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala Ala
 1 5 10 15

Asp Glu Ala Ala Gly Pro Ala Thr His Ala Pro Ser Ser Pro Glu Gly
 20 25 30

Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Thr Tyr
 35 40 45

Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Thr Gly
 50 55 60

Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val Asn
 65 70 75 80

Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala Ala
 85 90 95

Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Thr Gln
 100 105 110

Lys Tyr Phe Val Thr Leu Thr Tyr Gln Phe Lys Gly Gly Leu Gln Tyr
 115 120 125

Phe Val Gly Lys Lys Thr Val Ile Phe Leu Ser Gly Tyr Val Ser Thr

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130	135	140
Ile Gly Gly Arg Lys	Ile Ser Gln Val Lys Val	Lys His Arg Leu Pro
145	150	155 160
Thr Pro Gln Thr Ala Ser Val	Gly Ala Glu Gly Ser Gly Ser Gly Ala	
	165 170	175
Ala Ala Thr Ser Ser Ala Pro Pro Ala		
	180 185	

<210> SEQ ID NO 9
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 9

Gly Gly Lys Thr Leu Asn Ala Val Gln Glu Lys Lys Pro Pro Glu Ala
1 5 10 15

Pro Ala Ala Asp Glu Ala Ala

20

<210> SEQ ID NO 10
 <211> LENGTH: 324
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 10

Met Lys Lys Arg Ile Arg Val Phe Ala Phe Ala Val Phe Met Leu Gly
1 5 10 15
Leu Pro Ser Val Ser Phe Ala Ser Pro Gln Pro Val Asp Phe Ser Tyr
20 25 30
His Glu Gly Ala Ser Gly Phe Phe Ala Ser Val Gln Tyr Lys Tyr Gly
35 40 45
Ala Pro Tyr Phe Gly Ser Leu Thr Leu Glu Ser Gly Gly Lys Thr Leu
50 55 60
Asn Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala
65 70 75 80
Ala Asp Glu Ala Ala Glu Pro Ala Thr Pro Ala Pro Ser Ser Pro Glu
85 90 95
Gly Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Ala
100 105 110
Tyr Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Thr
115 120 125
Gly Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val
130 135 140
Asn Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala
145 150 155 160
Ala Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Ala
165 170 175
Gln Lys Tyr Phe Val Thr Leu Glu Asn Arg Asp Val Ala Ile Thr Ser
180 185 190
Leu Val Ala Asn Ala Cys Tyr Asp Met Met Pro Ala Thr Ser Ser Ile
195 200 205
Ala Pro Ser Ala Cys Val Gly Val Gly Val Ser Phe Ala Lys Leu Leu
210 215 220

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Gly Val Leu Glu Gln Arg Leu Thr Tyr Gln Phe Lys Gly Gly Ser Gln
 225 230 235 240

Tyr Phe Val Gly Lys Lys Thr Val Ile Phe Leu Ser Gly Tyr Val Ser
 245 250 255

Thr Ile Gly Gly Arg Lys Ile Thr Gln Val Lys Val Lys His Arg Leu
 260 265 270

Pro Thr Pro Gln Thr Ala Ser Val Gly Ala Glu Gly Ser Gly Ala Gly
 275 280 285

Ala Ala Ala Thr Ser Ser Ala Pro Pro Ala Pro Ile His Leu Leu Tyr
 290 295 300

Pro Asp Ala Asn Leu Ser Leu Ala Tyr Tyr Gly Phe Glu Leu Gly Val
 305 310 315 320

Arg Leu Val Phe

<210> SEQ ID NO 11
 <211> LENGTH: 975
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 11

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atgaagaaga gaatccgggt ttctcgcttt gcagtgttca tgcttgggtt gccctccgta    60
tcatttgctt ctccacaacc cgtggatttt tcgtaccacg aggggtgcac cggtcttttt    120
gccagcgttc agtataagta cgtgacaccc tatttcggaa gccttacact ggaaagcggc    180
gggaagacgc tgaatcttgt gagcgcggtg caggaaaaga aacccccgga agcccccgca    240
gttgacgaag ctgctgaacc tgccaccctt gctccctcaa gccctgaagg gtttggttca    300
tctaccgatg attttcaagg taggtactcg ccaacctatt taaaggacgc aggagccttt    360
tcaataacag cgggttatat caccggtatt atgagatttg aagcagaggc tatgcgttcg    420
cgtttccagg taaatggcag taaatggaat cctgtagaga acgcttatat atttgccgct    480
gctaaaccca gtgagaatat atcgtaccct gctcagatac tggaggcaca aaagtacttc    540
gtcaccttgg aaaacaggga tgttgccatc acttcgctgg tggcaaatgc ctgctacgac    600
atgatgccag caacctctag catcgcacct agtgcggtgc tgggtgtagg ggtagcttt    660
gccaactgt taggtgttct ggaacaaagg ctaacctatc aattcaaagg tggattgcaa    720
tattttgtcg gcaaaaagac cgtcatcttc ctatctggat acgtatccac aataggtgga    780
aggaaaatca ctcaggtaaa agtgaaacat cgtttgcca cgctcagac cgcgtcagtt    840
gggtgcagaag gcagtggagc aggtgctgct gcaacatctt ctgctcccc agccccatt    900
cacctgttgt acccagatgc aaatttatcg ctagegtact acgggtttga gcttgggggtg    960
cgtcttgctt tctaa                                     975
  
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<210> SEQ ID NO 12
 <211> LENGTH: 975
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 12

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atgaagaaga gaatccgggt ttctcgcttt gcagtgttca tgcttgggtt gccctccgta    60
tcatttgctt ctccacaacc cgtggatttt tcgtaccacg aggggtgcac cggtcttttt    120
gccagcgttc agtataagta cgtgacaccc tatttcggaa gccttacact ggaaagcggc    180
  
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gggaagattc tgaatcttgt gagcgcggtg caggaaaaga aacccccgga agcccccgca    240
gctgacgaag ctgctggacc tgccaccat gctccctcaa gccctgaagg gtttggttca    300
tctaccgatg attttcaagg taggtactcg ccaacctatt taaaggacgc aggagccttt    360
tcaataacag cgggttatat caccggtatt atgagatttg aagcagaggc tatgcttcg    420
cgtttccagg taaatggcag taaatggaat cctgtagaga acgcttatat atttgccgct    480
gctaaacca gtgagaatat atcgctaccct gctcagatac tggagacaca aaagtacttc    540
gtcaccttgg aaaacagga tgttgccatc acttcgctgg tggcaatgc ctgctacgac    600
atgatgccag caacctctag catcgacact agtgcgtgcg tgggtgtagg ggtagcttt    660
gccaactgt taggtgttct ggaacaaagg ctaacctatc aattcaaagg tggattgcaa    720
tattttgtcg gcaaaaagac cgtcatcttc ctatctggat acgtatccac aataggtgga    780
aggaaaatct ctcaggtaaa agtgaaacat cgtttgccca cgcctcagac cgcgtcagtt    840
ggtgcagaag gcagtggatc aggtgctgct gcaacatctt ctgctcccc agccctcatc    900
cacctgttgt acccagatgc aaatttatcg ctagegtact acgggtttga gcttggggtg    960
cgtcttgttt tctaa                                                    975

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<210> SEQ ID NO 13
<211> LENGTH: 975
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 13

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atgaagaaga gaatccgggt tttcgcgttt gcagtgttca tgcttgggtt gccctccgta    60
tcatttgctt ctccacaacc cgtggatttt tcgtaccacg aggggtgcac cggtcttttt    120
gccagcgttc agtataagta cgggtgcacc tatttcggaa gccttacct ggaaagcggc    180
gggaagacgc tgaatcttgt gagcgcggtg caggaaaaga aacccccgga agcccccgca    240
gctgacgaag ctgctgaacc tgccaccat gctccctcaa gccctgaagg gtttggttca    300
tctaccgatg attttcaagg taggtactcg ccagcctatt taaaggacgc aggagccttt    360
tcaataacag cgggttatat caccggtatt atgagatttg aagcagaggc tatgcttcg    420
cgtttccagg taaatggcag taaatggaat cctgtagaga acgcttatat atttgccgct    480
gctaaacca gtgagaatat atcgctaccct gctcagatac tggaggcaca aaagtacttc    540
gtcaccttgg aaaacagga tgttgccatc acttcgctgg tggcaatgc ctgctacgac    600
atgatgccag caacctctag catcgacact agtgcgtgcg tgggtgtagg ggtagcttt    660
gccaactgt taggtgttct ggaacaaagg ctaacctatc aattcaaagg tggatcgcaa    720
tattttgtcg gcaaaaagac cgtcatcttc ctatctggat acgtatccac aataggtgga    780
aggaaaatca ctcaggtaaa agtgaaacat cgtttgccca cgcctcagac cgcgtcagtt    840
ggtgcagaag gcagtggagc aggtgctgct gcaacatctt ctgctcccc agccccatt    900
cacctgttgt acccagatgc aaatttatcg ctagegtact acgggtttga gcttggggtg    960
cgtcttgttt tctaa                                                    975

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<210> SEQ ID NO 14
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 14

ctgaatcttg tgagcgcggt gcaggaaaag aaacccccgg aagccccgc agctgacgaa	60
gctgctgaac ctgccacccc tgctccctca agccctgaag ggtttggttc atctaccgat	120
gattttcaag gtaggtactc gccaacctat ttaaaggacg caggagcctt ttcaataaca	180
gcgggttata ccaccggtat tatgagattt gaagcagagg ctatgcgttc gcgtttccag	240
gtaaatggca gtaaattggaa tcctgtagag aacgcttata tatttgccgc tgctaaaccc	300
agtgagaata tatcgtaacc tgctcagata ctggaggcac aaaagtactt cgtaaccttg	360

<210> SEQ ID NO 15

<211> LENGTH: 204

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 15

ctaacctatc aattcaaagg tggattgcaa tttttgtcg gcaaaaagac cgtaactctt	60
ctatctggat acgtatccac aataggtgga aggaaaatca ctcaggtaaa agtgaacat	120
cgtttgtcca cgcctcagac cgcgtcagtt ggtgcagaag gcagtggagc aggtgctgct	180
gcaacatctt ctgctcccc agcc	204

<210> SEQ ID NO 16

<211> LENGTH: 564

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 16

ctgaatcttg tgagcgcggt gcaggaaaag aaacccccgg aagccccgc agctgacgaa	60
gctgctgaac ctgccacccc tgctccctca agccctgaag ggtttggttc atctaccgat	120
gattttcaag gtaggtactc gccaacctat ttaaaggacg caggagcctt ttcaataaca	180
gcgggttata ccaccggtat tatgagattt gaagcagagg ctatgcgttc gcgtttccag	240
gtaaatggca gtaaattggaa tcctgtagag aacgcttata tatttgccgc tgctaaaccc	300
agtgagaata tatcgtaacc tgctcagata ctggaggcac aaaagtactt cgtaaccttg	360
ctaacctatc aattcaaagg tggattgcaa tttttgtcg gcaaaaagac cgtaactctt	420
ctatctggat acgtatccac aataggtgga aggaaaatca ctcaggtaaa agtgaacat	480
cgtttgtcca cgcctcagac cgcgtcagtt ggtgcagaag gcagtggagc aggtgctgct	540
gcaacatctt ctgctcccc agcc	564

<210> SEQ ID NO 17

<211> LENGTH: 51

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 17

gcgggtgcagg aaaagaaacc ccggaagcc cccgcagctg acgaagctgc t	51
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<210> SEQ ID NO 18

<211> LENGTH: 19

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 18

ctgaatcttg tgagcgcg          19

<210> SEQ ID NO 19
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 19

caagtgacg aagtactttt gtg          23

<210> SEQ ID NO 20
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 20

ctaacctatc aattcaaagg tggattg          27

<210> SEQ ID NO 21
<211> LENGTH: 406
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 21

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
1      5      10      15

Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp
20     25     30

Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
35     40     45

Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
50     55     60

Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
65     70     75     80

Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
85     90     95

Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr
100    105    110

Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe
115    120    125

Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp
130    135    140

Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp
145    150    155    160

Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu
165    170    175

Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp
180    185    190

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Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala Ala Gly Ser Trp
 195 200 205
 Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr Ala Glu Phe Ser
 210 215 220
 Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala
 225 230 235 240
 Trp Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu Asp Leu Ser Ile
 245 250 255
 Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly
 260 265 270
 Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu Ile Arg Ala
 275 280 285
 Val Ser Thr Thr Ser Val Met Leu Asn Gly Cys Tyr Asp Leu Gln Ser
 290 295 300
 Glu Gly Phe Ser Ile Val Pro Tyr Ala Cys Leu Gly Val Gly Ala Asn
 305 310 315 320
 Phe Val Gly Ile Val Asp Gly His Val Thr Pro Lys Leu Ala Tyr Lys
 325 330 335
 Val Lys Ala Gly Leu Ser Tyr Glu Leu Ser Pro Glu Ile Ser Met Phe
 340 345 350
 Ala Gly Gly Phe Tyr His Arg Val Leu Gly Glu Gly Glu Tyr Asp Asp
 355 360 365
 Leu Pro Val Gln Arg Leu Val Asp Asp Ala Thr Thr Asn Lys Thr Lys
 370 375 380
 Glu Phe Ala Lys Ala Ser Phe Lys Met Ala Tyr Thr Gly Ala Glu Ile
 385 390 395 400
 Gly Val Arg Ser Ala Phe
 405

<210> SEQ ID NO 22
 <211> LENGTH: 406
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 22

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
 1 5 10 15
 Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp
 20 25 30
 Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
 35 40 45
 Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
 50 55 60
 Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
 65 70 75 80
 Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
 85 90 95
 Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr
 100 105 110
 Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe
 115 120 125
 Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp
 130 135 140

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Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp
 145 150 155 160

Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu
 165 170 175

Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp
 180 185 190

Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala Ala Gly Ser Trp
 195 200 205

Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr Ala Glu Phe Ser
 210 215 220

Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala
 225 230 235 240

Arg Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu Asp Leu Ser Ile
 245 250 255

Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly
 260 265 270

Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu Ile Arg Ala
 275 280 285

Val Ser Thr Thr Ser Val Met Leu Asn Gly Cys Tyr Asp Leu Gln Ser
 290 295 300

Glu Gly Phe Ser Ile Val Pro Tyr Ala Cys Leu Gly Val Gly Ala Asn
 305 310 315 320

Phe Val Gly Ile Val Asp Gly His Val Thr Pro Lys Leu Ala Tyr Lys
 325 330 335

Val Lys Ala Gly Leu Ser Tyr Glu Leu Ser Pro Glu Ile Ser Met Phe
 340 345 350

Ala Gly Gly Phe Tyr His Arg Val Leu Gly Glu Gly Glu Tyr Asp Asp
 355 360 365

Leu Pro Val Gln Arg Leu Val Asp Asp Ala Thr Thr Asn Lys Thr Lys
 370 375 380

Glu Phe Ala Lys Ala Ser Phe Lys Met Ala Tyr Thr Gly Ala Glu Ile
 385 390 395 400

Gly Val Arg Phe Ala Phe
 405

<210> SEQ ID NO 23
 <211> LENGTH: 400
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 23

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
 1 5 10 15

Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp
 20 25 30

Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
 35 40 45

Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
 50 55 60

Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
 65 70 75 80

Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
 85 90 95

Lys	Phe	Lys	Asn	Asn	Pro	Ile	Val	Ala	Leu	Glu	Gly	Ser	Val	Gly	Tyr
			100					105					110		
Ser	Ile	Gly	Val	Ala	Arg	Val	Glu	Leu	Glu	Ile	Gly	Tyr	Glu	Gln	Phe
		115					120					125			
Lys	Thr	Lys	Gly	Ile	Arg	Asp	Thr	Gly	Ser	Lys	Glu	Glu	Glu	Ala	Asp
		130				135					140				
Ala	Val	Tyr	Leu	Leu	Ala	Lys	Lys	Leu	Pro	His	Thr	Leu	Val	Ser	Asp
145					150					155					160
Gln	Ser	Asp	Lys	Phe	Leu	Glu	Glu	Leu	Lys	Asn	Thr	Lys	Ala	Ala	Glu
				165					170					175	
Ile	Val	Lys	Phe	Ala	Glu	Ala	Val	Gly	Thr	Ser	Ala	Lys	Asp	Ile	Asp
			180					185					190		
Lys	Lys	Val	Cys	Lys	Lys	Thr	Glu	Asn	Thr	Glu	Asp	Ser	Trp	Lys	Cys
		195					200					205			
Thr	Gln	Thr	Gly	Asn	Asp	Gly	Ser	Asp	Lys	Glu	Phe	Ser	Lys	Ile	Phe
210						215					220				
Thr	Lys	Lys	Asn	Val	Asp	Thr	Ser	Gly	Lys	Ala	Trp	Pro	Asn	Gly	Ser
225					230					235					240
Asp	Ala	Ala	Lys	Ala	Glu	Asp	Leu	Ser	Thr	Ala	Leu	Asn	Arg	Glu	Leu
				245					250					255	
Thr	Ser	Ala	Glu	Lys	Asn	Lys	Val	Ala	Gly	Leu	Leu	Thr	Arg	Thr	Ile
			260					265					270		
Ser	Gly	Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val	Ser	Thr	Thr	Ser	Val
		275					280					285			
Met	Leu	Asn	Gly	Cys	Tyr	Asp	Leu	Gln	Ser	Glu	Gly	Phe	Ser	Ile	Val
290						295					300				
Pro	Tyr	Ala	Cys	Leu	Gly	Val	Gly	Ala	Asn	Phe	Val	Gly	Ile	Val	Asp
305					310					315					320
Gly	His	Val	Thr	Ser	Lys	Leu	Ala	Tyr	Lys	Val	Lys	Ala	Gly	Leu	Ser
				325					330					335	
Tyr	Glu	Leu	Ser	Pro	Glu	Ile	Ser	Met	Phe	Ala	Gly	Gly	Phe	Tyr	His
			340					345					350		
Arg	Val	Leu	Gly	Glu	Gly	Glu	Tyr	Asp	Asp	Leu	Pro	Val	Gln	Arg	Leu
		355					360					365			
Val	Asp	Asp	Ala	Thr	Thr	Asn	Lys	Thr	Lys	Glu	Phe	Ala	Lys	Ala	Ser
		370				375					380				
Phe	Lys	Met	Ala	Tyr	Thr	Gly	Ala	Glu	Ile	Gly	Val	Arg	Phe	Ala	Phe
385					390					395					400

<400> SEQUENCE: 24

Met	Lys	Glu	Arg	Lys	Leu	Ala	Leu	Ser	Gly	Ala	Val	Ala	Met	Thr	Val
1				5					10					15	
Leu	Val	Ser	Thr	Ala	Gly	Thr	Gly	Thr	Ala	Ala	Gly	Ser	Asp	Val	Asp
				20				25					30		
Tyr	Val	Ser	Lys	Phe	Gly	Glu	Gly	Ser	Phe	Tyr	Val	Gly	Leu	Asn	Tyr
				35			40					45			
Ser	Pro	Ala	Phe	Ser	Lys	Ile	Asn	Gly	Phe	Glu	Ile	Arg	Glu	Ser	Thr
	50					55					60				

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Gly	Glu	Thr	Ala	Ala	Val	Tyr	Pro	Tyr	Met	Lys	Asp	Gly	Thr	Arg	Val	65	70	75	80
Glu	Trp	Lys	Ala	Glu	Lys	Phe	Asp	Trp	Asn	Thr	Pro	Asp	Pro	Arg	Ile	85	90	95	
Lys	Phe	Lys	Asn	Asn	Pro	Ile	Val	Ala	Leu	Glu	Gly	Ser	Val	Gly	Tyr	100	105	110	
Ser	Ile	Gly	Val	Ala	Arg	Val	Glu	Leu	Glu	Ile	Gly	Tyr	Glu	Gln	Phe	115	120	125	
Lys	Thr	Lys	Gly	Ile	Arg	Asp	Thr	Gly	Ser	Lys	Glu	Glu	Glu	Ala	Asp	130	135	140	
Ala	Val	Tyr	Leu	Leu	Ala	Lys	Lys	Leu	Pro	His	Thr	Leu	Val	Ser	Asp	145	150	155	160
Gln	Ser	Asp	Lys	Phe	Leu	Glu	Glu	Leu	Lys	Asn	Thr	Lys	Ala	Ala	Glu	165	170	175	
Ile	Val	Lys	Phe	Ala	Glu	Ala	Val	Gly	Thr	Ser	Ala	Lys	Asp	Ile	Asp	180	185	190	
Lys	Lys	Val	Cys	Lys	Lys	Thr	Glu	Asn	Thr	Glu	Asp	Ser	Trp	Lys	Cys	195	200	205	
Thr	Gln	Thr	Gly	Asn	Asp	Gly	Gly	Asp	Lys	Glu	Phe	Ser	Lys	Ile	Phe	210	215	220	
Thr	Lys	Lys	Asn	Val	Asp	Thr	Ser	Gly	Lys	Ala	Trp	Pro	Asn	Gly	Ser	225	230	235	240
Asp	Ala	Ala	Lys	Ala	Glu	Asp	Leu	Ser	Thr	Ala	Leu	Asn	Arg	Glu	Leu	245	250	255	
Thr	Ser	Ala	Glu	Lys	Asn	Lys	Val	Ala	Gly	Leu	Leu	Thr	Arg	Thr	Ile	260	265	270	
Ser	Gly	Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val	Ser	Thr	Thr	Ser	Val	275	280	285	
Met	Leu	Asn	Gly	Cys	Tyr	Asp	Leu	Gln	Ser	Glu	Gly	Phe	Ser	Ile	Val	290	295	300	
Pro	Tyr	Ala	Cys	Leu	Gly	Val	Gly	Ala	Asn	Phe	Val	Gly	Ile	Val	Asp	305	310	315	320
Gly	His	Val	Thr	Pro	Lys	Leu	Ala	Tyr	Lys	Val	Lys	Ala	Gly	Leu	Ser	325	330	335	
Tyr	Glu	Leu	Ser	Pro	Glu	Ile	Ser	Met	Phe	Ala	Gly	Gly	Phe	Tyr	His	340	345	350	
Arg	Val	Leu	Gly	Glu	Gly	Glu	Tyr	Asp	Asp	Leu	Pro	Val	Leu	Arg	Leu	355	360	365	
Val	Asp	Asp	Ala	Thr	Thr	Asn	Lys	Thr	Lys	Glu	Phe	Ala	Lys	Ala	Ser	370	375	380	
Phe	Lys	Met	Ala	Tyr	Thr	Gly	Ala	Glu	Ile	Gly	Val	Arg	Phe	Ala	Phe	385	390	395	400

<210> SEQ ID NO 25

<211> LENGTH: 280

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 25

Met	Lys	Glu	Arg	Lys	Leu	Ala	Leu	Ser	Gly	Ala	Val	Ala	Met	Thr	Val	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Leu	Val	Ser	Thr	Ala	Gly	Thr	Gly	Thr	Ala	Ala	Gly	Ala	Asp	Val	Asp	20	25	30	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	--

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Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
 35 40 45
 Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
 50 55 60
 Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
 65 70 75 80
 Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
 85 90 95
 Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr
 100 105 110
 Ser Ile Gly Ile Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe
 115 120 125
 Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp
 130 135 140
 Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp
 145 150 155 160
 Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu
 165 170 175
 Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp
 180 185 190
 Gly Lys Val Cys Lys Lys Thr Gly Asn Glu Ala Asp Ser Trp Lys Cys
 195 200 205
 Thr Gln Thr Gly Asn Gly Ser Gly Asn Ala Thr Glu Phe Ser Lys Ile
 210 215 220
 Phe Thr Lys Lys Asn Val Asp Ala Glu Gly Lys Gly Lys Ala Trp Pro
 225 230 235 240
 Asn Gly His Thr Asp Ser Ala Ala Lys Ala Glu Asp Leu Ser Thr Ala
 245 250 255
 Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly Leu
 260 265 270
 Leu Thr Arg Thr Ile Ser Gly Gly
 275 280

<210> SEQ ID NO 26
 <211> LENGTH: 86
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 26

Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val Gly
 1 5 10 15
 Thr Ser Ala Lys Asp Ile Asp Gly Lys Val Cys Lys Lys Gly Gly Ser
 20 25 30
 Gly Asn Ala Ala Gly Ser Trp Lys Cys Thr Gln Thr Gly Ser Asn Gly
 35 40 45
 Val Ser Thr Ala Glu Phe Ser Lys Ile Phe Phe Lys Ala Asp Val Asn
 50 55 60
 Thr Asp Asn Lys Gly Lys Ala Trp Pro Asn Gly Asn Asn Asp Ala Ala
 65 70 75 80
 Lys Ala Glu Asp Leu Ser
 85

<210> SEQ ID NO 27
 <211> LENGTH: 84

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 27

Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val Gly
1 5 10 15
Thr Ser Ala Lys Asp Ile Asp Lys Lys Val Cys Lys Lys Thr Asp Asn
20 25 30
Thr Glu Gly Ser Trp Lys Cys Thr Gln Thr Gly Asn Asp Gly Gly Asp
35 40 45
Lys Glu Phe Ser Lys Thr Phe Thr Lys Thr Gly Val Asn Glu Ala Thr
50 55 60
Lys Gly Lys Ala Trp Pro Asn Gly His Thr Asp Ser Ala Ala Lys Ala
65 70 75 80
Glu Asp Leu Ser

<210> SEQ ID NO 28
<211> LENGTH: 84
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 28

Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val Gly
1 5 10 15
Thr Ser Ala Lys Asn Ile Asp Lys Lys Val Cys Lys Lys Thr Gly Asn
20 25 30
Asp Ala Asn Ser Trp Lys Cys Leu Gln Thr Gly Arg Asp Asp Ser Thr
35 40 45
Ser Gly Lys Lys Phe Ser Glu Ile Phe Thr Lys Ala Asp Val Asn Thr
50 55 60
Asp Asn Lys Gly Lys Ala Trp Pro Asn Gly Asn Glu Ala Ala Lys Ala
65 70 75 80
Glu Asp Leu Ser

<210> SEQ ID NO 29
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 29

Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val Gly
1 5 10 15
Thr Ser Ala Lys Asn Ile Asp Lys Lys Val Cys Lys Lys Thr Gly Asn
20 25 30
Asp Ala Asn Ser Trp Lys Cys Glu Gln Thr Gly Ser Gly Ala Glu Thr
35 40 45
Ser Ala Lys Ala Phe Ser Glu Ile Phe Thr Lys Ala Gly Val Asn Glu
50 55 60
Ala Thr Lys Gly Lys Ala Trp Pro Asn Gly His Thr Gly Gly Ala Ala
65 70 75 80
Lys Ala Glu Asp Leu Ser
85

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<210> SEQ ID NO 30
 <211> LENGTH: 1221
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 30

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atgaagggaaa gaaaacttgc gctaagtgga gcggtggcga tgacagtttt ggtgtcgact    60
gctggtaccg ggactgcggc agggctcggac gtggactatg taagtaagtt cggtgagggc    120
agcttctacg taggtctaaa ctatagtccg gcgtttagta agataaatgg gtttgagata    180
agagagagta ccggggaaac tgcggcagta tatccgtaca tgaagatgg aactagagt    240
gagtggaaaag ctgagaagtt cgactggaac acaccagatc cgaggattaa gtttaaaaac    300
aatcctatcg tggcgtaga aggaagtgtg ggctacagta tcggggtagc gagagtagaa    360
ctggagatcg gctatgaaca gttcaagacg aaaggaataa gagatacggg aagtaaggaa    420
gaagaagctg atgccgtgta cctgttggct aagaagctac cgcataccct ggtgagtgac    480
cagagcgata aattcctgga ggagctgaag aatacgaaaag cggcggagat cgtaaattt    540
gctgaggtcg ttggcacatc ggcaaaggat attgatggaa aggtttgtaa gaaggcggc    600
agcggcaatg ccgcgggcag ctggaagtgt acgcagactg gcagcaacgg cgtcagcacc    660
gcagagttca gtaaaatatt tacgaaggca gacgtaaata ctgacaacaa aggcaaagca    720
tggcctaacg ggaacaacga cgctgcgaaa gcggaagacc taagtattgc gttgaataga    780
gaactaacca gcgccgaaaa gaacaaggta gctggcctac taaccaggac tatatccggt    840
ggtgaggtag tggagatccg tgcggtgtcg acaacgtcag taatgttgaa tggttgttat    900
gatctgcaga gtgaaggggt tagtatagta cttatgcat gtcttggtgt aggtgctaac    960
ttcgttgga ttgttgacgg acacgtcact cctaaactgg cttacaaggt caaggctggt    1020
ttgagttatg agttgtcgcc ggaatatctca atgttcgctg gtgggttcta tcatcgggtg    1080
ctgggtgaag gtgagtaga tgatctgcca gtgcagaggc ttgtagacga tgcgactacg    1140
aacaagacta aagagttcgc taaagcgtcg ttcaagatgg cgtacactgg tgctgaaatc    1200
ggtgttaggt ctgcgttcta a                                     1221

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<210> SEQ ID NO 31
 <211> LENGTH: 1221
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 31

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atgaagggaaa gaaaacttgc gctaagtgga gcggtggcga tgacagtttt ggtgtcgact    60
gctggtaccg ggactgcggc agggctcggac gtggactatg taagtaagtt cggtgagggc    120
agcttctacg taggtctaaa ctatagtccg gcgtttagta agataaatgg gtttgagata    180
agagagagta ccggggaaac tgcggcagta tatccgtaca tgaagatgg aactagagt    240
gagtggaaaag ctgagaagtt cgactggaac acaccagatc cgaggattaa gtttaaaaac    300
aatcctatcg tggcgtaga aggaagtgtg ggctacagta tcggggtagc gagagtagaa    360
ctggagatcg gctatgaaca gttcaagacg aaaggaataa gagatacggg aagtaaggaa    420
gaagaagctg atgccgtgta cctgttggct aagaagctac cgcataccct ggtgagtgac    480
cagagcgata aattcctgga ggagctgaag aatacgaaaag cggcggagat cgtaaattt    540

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gctgaggctg ttggcacatc ggcaaaggat attgatggaa aggtttgtaa gaaggcgccg 600
agcggcgaatg ccgcgggcag ctggaagtgt acgcagactg gcagcaacgg cgtcagcacc 660
gcagagttca gtaaaatatt tacgaaggca gacgtaaata ctgacaacaa aggcaaagca 720
cggcctaacg ggaacaacga cgtgcgaaa gcggaagacc taagtattgc gttgaataga 780
gaactaacca gcgccgaaaa gaacaaggta gctggcctac taaccaggac tatatccggt 840
ggtgaggtag tggagatccg tgcggtgtcg acaacgtcag taatggtgaa tggttgttat 900
gatctgcaga gtgaagggtt tagtatagta cttatgcat gtcttggtgt aggtgctaac 960
ttcgttgcca ttgttgacgg acacgtcact cctaaactgg cttacaaggt caaggctggt 1020
ttgagttatg aattgtcgcc ggaatctca atgttcgctg gtgggttcta tcatcggtg 1080
ctgggtgaag gtgagtaga tgatctgcca gtgcagaggc ttgtagacga tgcgactacg 1140
aacaagacta aagagttcgc taaagcgtcg ttcaagatgg cgtacactgg tgctgaaatc 1200
ggtgttaggt ttcggttcta a 1221

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<210> SEQ ID NO 32
<211> LENGTH: 1203
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 32

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atgaagggaaa gaaaacttgc gctaagtgga gcggtggcga tgacagtttt ggtgtcgact 60
gctgttaccg ggactgcggc aggggtcggac gtggactatg taagtaagtt cggtgagggc 120
agcttctacg taggtctaaa ctatagtccg gcgtttagta agataaatgg gtttgagata 180
agagagagta ccggggaaac tgcggcagta tatccgtaca tgaaagatgg aactagagtg 240
gagtggaagc ctgagaagtt cgactggaac acaccagatc cgaggattaa gtttaaaaac 300
aatcctatcg tggcgtaga aggaagtgtg ggctacagta tcggggtagc gagagtagaa 360
ctggagatcg gctatgaaca gttcaagacg aaaggaataa gagatacggg aagtaaggaa 420
gaagaagctg atgccgtgta cctgttggct aagaagctac cgcataccct ggtgagtgac 480
cagagcgata aattcctgga ggagctgaag aatacgaagc cggcggagat cgtaagttt 540
gctgaggctg tcggtacatc ggcaaaggat attgataaga aggtttgtaa gaagactgaa 600
aatacagaag acagtgtgaa gtgtacgcag actggcaacg acggcagcga caaggagttc 660
agtaaaatat ttacgaagaa aaacgtagat actagcggca aagcatggcc taacggaagc 720
gacgcccgca aagcggaaga cctaagtact gcgctgaata gagaactaac cagcccgcaa 780
aagaacaagg tagctggcct actaaccagg actatatccg gtggtgaggt agtggagatc 840
cgtgcggtgt cgacaacgtc agtaatgttg aatggttgtt atgatctgca gagtgaaggg 900
tttagtatag taccttatgc atgtcttggg ttaggtgcta acttcgttgg cattgttgac 960
ggacacgtca cttctaaact ggcttacaag gtcaaggctg gtttgagtta tgagttgtcg 1020
ccggaatatc caatgttcgc tgggtgggtc tatcatcggg tgctgggtga aggtgagtag 1080
gatgatctgc cagtgcagag gctttagtag gatgcgacta cgaacaagac taaagagttc 1140
gctaaagcgt cgttcaagat ggcgtacact ggtgctgaaa tcggtgttag gtttgcgttc 1200
taa 1203

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<210> SEQ ID NO 33

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<211> LENGTH: 1203
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 33
atgaaggaaa gaaaacttgc gctaagtgga gcggtggcga tgacagtttt ggtgtcgact    60
gctggtaccg ggactcggcg agggtcggac gtggactatg taagtaagtt cggtgagggc    120
agcttctacg taggtctaaa ctatagtccg gcgttttagta agataaatgg gtttgagata    180
agagagagta ccggggaaac tgcggcagta tatccgtaca tgaaagatgg aactagagtg    240
gagtggaaag ctgagaagtt cgactggaac acaccagatc cgaggattaa gtttaaaaac    300
aatcctatcg tggcgtaga aggaagtgtg ggctacagta tcggggtagc gagagtagaa    360
ctggagatcg gctatgaaca gttcaagacg aaaggaataa gagatacggg aagtaaggaa    420
gaagaagctg atgccgtgta cctattggct aagaagctac cgcataccct ggtgagtgac    480
cagagcgata aattcctgga ggagctgaag aatacgaagc cggcggagat cgtaagttt    540
gctgaggctg ttggtacatc ggcaaaggat attgataaga aggtttgtaa gaagactgaa    600
aatacagaag acagttggaa gtgtacgcag actggcaacg acggcggcga caaggagttc    660
agtaaaatat ttacgaagaa aaacgtagat actagcggca aagcatggcc taacggaagc    720
gacgccgcga aagcgggaaga cctaagtact gcgctgaata gagaactaac cagcccgcaa    780
aagaacaagg tagctggcct actaaccagg actatatccg gtggtgaggt agtggagatc    840
cgtgcggtgt cgacaacgtc agtaatgttg aatggttgtt atgatctgca gagtgaaggg    900
tttagtatag taccttatgc atgtcttggt gtaggtgcta acttcgttgg cattgttgac    960
ggacacgtca ctctaaact ggcttacaag gtcaaggctg gtttgagtta tgagttgtcg    1020
ccggaatct caatgttcgc tggtggttc tatcatcggg tgctgggtga aggtgagtag    1080
gatgatctgc cagtgtgtag gctttagtag gatgcgacta cgaacaagac taaagagttc    1140
gctaaagcgt cgttcaagat ggcgtacact ggtgctgaaa tcggtgttag gtttgcgttc    1200
taa                                                1203

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<210> SEQ ID NO 34
<211> LENGTH: 260
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 34
gaagaatacg aaagcggcgg agatcgtaa atttgctgag gctgttggca catcgcaaaa    60
ggatattgat ggaaggttt gtaagaaggc cggcagcggc aatgcccgcg gcagctggaa    120
gtgtacgcag actggcagca acggcgctcag caccgcagag ttcagtaaaa tatttacgaa    180
ggcagacgta aatactgaca acaaaggcaa agcatggcct aacgggaaca acgacgctgc    240
gaaagcggaa gacctaagta                                                260

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<210> SEQ ID NO 35
<211> LENGTH: 254
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 35

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gaagaatacg aaagcggcgg agatcgtaa atttgctgag gctgttgga catcgcaaa	60
ggatattgat aagaaggttt gtaagaagac tgacaataca gaaggcagtt ggaagtgtac	120
gcagactggc aacgacggcg gcgacaagga gttagtaaa acatttacga agacggcggt	180
gaatgagggc accaagggca aagcatggc taacgggcac accgacagcg ccgcgaaagc	240
ggaagaccta agta	254

<210> SEQ ID NO 36
 <211> LENGTH: 254
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 36

gaagaatacg aaagcggcgg agatcgtaa atttgctgag gctgttgga catcgcaaa	60
gaatattgat aagaaggttt gtaagaagac tggaaatgac gcgaacagtt ggaagtgtt	120
gcagactggc agagacgaca gcacgtcggg gaaaaagttc agtgaaatat ttacgaaggc	180
agacgtaaat actgacaaca aaggcaaac atggcctaac gggaacgaag ccgcgaaagc	240
ggaagaccta agta	254

<210> SEQ ID NO 37
 <211> LENGTH: 260
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 37

gaagaatacg aaagcggcgg agatcgtaa atttgctgag gctgttgga catcgcaaa	60
gaatattgat aagaaggttt gtaagaagac tggaaatgac gcgaacagtt ggaagtgcga	120
gcagactggc agcggcgccg agacaagcgc caaggcggtc agtgaaatat ttacgaaggc	180
ggcggtgaat gaggccacca agggcaaac atggcctaac gggcacaccg gcggcgcccg	240
gaaagcggaa gacctaagta	260

<210> SEQ ID NO 38
 <211> LENGTH: 842
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 38

atgaaggaaa gaaaacttgc gctaagtga ggggtggcga tgacagtttt ggtgtcgact	60
gctgttaccg ggactgcggc aggggcggac gtggactatg taagtaagtt cggtaggggc	120
agcttctacg taggtctaaa ctatagtccg gcgtttagta agataaatgg gtttgagata	180
agagagagta ccggggaaac tgcggcagta tatccgtaca tgaaagatgg aactagagtg	240
gagtggaaaag ctgagaagtt cgactggaac acaccagatc cgaggattaa gtttaaaaac	300
aatcctatcg tggcggttga aggaagtgtg ggctacagta tcgggatagc gagagtagaa	360
ctagagatcg gctatgaaca gttcaagacg aaaggaataa gagatacggg aagtaaggaa	420
gaagaagctg atgccgtgta cctgttggtc aagaagctac cgcataacct ggtgagtgac	480
cagagcgata aattcctgga ggagctgaag aatacgaag cggcggagat cgttaagttt	540

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gctgaggctg ttggtacatc ggcaaaggat attgatggaa aggtttgtaa gaagactgga    600
aatgaggcgg acagttggaa gtgtacgcag actggcaacg gcagcggcaa cgccacagag    660
tttagtaaaa tatttacgaa gaaaaacgta gatgctgagg gcaaaggcaa agcatggcct    720
aacgggcaca cgcacagcgc cgcgaaagcg gaagacctaa gtactgcgtt gaatagagaa    780
ctaaccagcg ccgaaaagaa caaggtagct ggcctactaa ccaggactat atccggtggc    840
ga                                                                    842

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<210> SEQ ID NO 39
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 39

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```

Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp Tyr Val Ser Lys Phe
1           5           10          15

```

```

Gly Glu

```

```

<210> SEQ ID NO 40
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 40

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```

Gly Thr Arg Val Glu Trp Lys Ala Glu
1           5

```

```

<210> SEQ ID NO 41
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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```

<400> SEQUENCE: 41

```

```

Lys Lys Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe Leu
1           5           10          15

```

```

Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu
20          25          30

```

```

Ala Val Gly Thr Ser Ala Lys Asp
35          40

```

```

<210> SEQ ID NO 42
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 42

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```

Ser Trp Lys Cys Thr Gln Thr Gly
1           5

```

```

<210> SEQ ID NO 43
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 43

Ala Ala Lys Ala Glu Asp Leu Ser Ile Ala Leu Asn Arg Glu Leu Thr
1 5 10 15

Ser Ala Glu Lys Asn Lys
20

<210> SEQ ID NO 44

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 44

Ala Thr Thr Asn Lys Thr Lys Glu Phe
1 5

<210> SEQ ID NO 45

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 45

Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp Tyr Val Ser Lys Phe
1 5 10 15

Gly Glu Gly Thr Arg Val Glu Trp Lys Ala Glu Lys Lys Leu Pro His
20 25 30

Thr Leu Val Ser Asp Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn
35 40 45

Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser
50 55 60

Ala Lys Asp Ser Trp Lys Cys Thr Gln Thr Gly Ala Ala Lys Ala Glu
65 70 75 80

Asp Leu Ser Ile Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn
85 90 95

Lys Ala Thr Thr Asn Lys Thr Lys Glu Phe
100 105

<210> SEQ ID NO 46

<211> LENGTH: 54

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 46

ggtaccggga ctgcggcagg gtcggacgtg gactatgtaa gtaagttcgg tgag

54

<210> SEQ ID NO 47

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 47

ggaactagag tggagtggaa agctgag

27

<210> SEQ ID NO 48

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<211> LENGTH: 120
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 48

aagaagctac cgcataccct ggtgagtgac cagagcgata aattcctgga ggagctgaag 60
aatacgaaaag cggcggagat cgttaaattt gctgaggctg ttggcacatc ggcaaaggat 120

<210> SEQ ID NO 49
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 49

agctggaagt gtacgcagac tggc 24

<210> SEQ ID NO 50
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 50

gctgcgaaaag cggaagacct aagtattgctg ttgaatagag aactaaccag cgccgaaaag 60
aacaag 66

<210> SEQ ID NO 51
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 51

gcgactacga acaagactaa agagtgc 27

<210> SEQ ID NO 52
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 52

ggtaccggga ctgcggc 17

<210> SEQ ID NO 53
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 53

ctcaccgaac ttacttacat agtccac 27

<210> SEQ ID NO 54
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 54

ggaactagag tggagtggaa agc 23

<210> SEQ ID NO 55
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 55

ctcagctttc cactcc 16

<210> SEQ ID NO 56
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 56

aagaagctac cgcataccct g 21

<210> SEQ ID NO 57
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 57

atcctttgcc gatgtaccaa c 21

<210> SEQ ID NO 58
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 58

agctggaagt gtacgcagac tg 22

<210> SEQ ID NO 59
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 59

gccagtctgc gtacacttcc 20

<210> SEQ ID NO 60
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 60

gctgcgaaag cggaagac 18

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<210> SEQ ID NO 61
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 61

cttgttcttt tcggcgctg 19

<210> SEQ ID NO 62
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 62

gcgactacga acaagactaa agag 24

<210> SEQ ID NO 63
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 63

gaactcttta gtcttggtcg tagtcg 26

<210> SEQ ID NO 64
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 64

gcggtgcagg aaaagaaac 19

<210> SEQ ID NO 65
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 65

agcagcttcg tcagctgc 18

<210> SEQ ID NO 66
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 66

aacatatgaa tcttgtagc gcgg 24

<210> SEQ ID NO 67
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 67

ggggatccgg ctgggggagc agaag

25

<210> SEQ ID NO 68

<211> LENGTH: 31

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 68

aagctagcca aggtgacgaa gtacttttgt g

31

<210> SEQ ID NO 69

<211> LENGTH: 35

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 69

aagctagcct aacctatcaa ttcaaaggtg gattg

35

<210> SEQ ID NO 70

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 70

ggccatgggt accgggactg cggc

24

<210> SEQ ID NO 71

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 71

ttcatatgct cagctttcca ctcc

24

<210> SEQ ID NO 72

<211> LENGTH: 35

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 72

ccctgcagct caccgaactt acttacatag tccac

35

<210> SEQ ID NO 73

<211> LENGTH: 31

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 73

ggctgcaggg aactagagtg gagggaaag c

31

<210> SEQ ID NO 74

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<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 74

aaggatccaa gaagctaccg cataccctg 29

<210> SEQ ID NO 75
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 75

ccgtcgacgc cagtctgcgt acacttcc 28

<210> SEQ ID NO 76
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 76

aagaattcat cctttgccga tgtaccaac 29

<210> SEQ ID NO 77
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 77

ttgaattcag ctggaagtgt acgcagactg 30

<210> SEQ ID NO 78
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 78

aaaagcttgc tgcgaaagcg gaagac 26

<210> SEQ ID NO 79
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 79

ccctcgagga actctttagt cttgttcgta gtcg 34

<210> SEQ ID NO 80
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 80

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ttggatccct tgttcttttc ggcgctg 27

<210> SEQ ID NO 81
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 81

aaggatccgc gactacgaac aagactaaag ag 32

<210> SEQ ID NO 82
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 82

attatgtatg atttacccta agttatctga g 31

<210> SEQ ID NO 83
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 83

gggatatcgg cggtgatagg g 21

<210> SEQ ID NO 84
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 84

ggtttggtgtt gctgggtgatt ggagg 25

<210> SEQ ID NO 85
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 85

gcaaacctaa caccmaaytc mccacc 26

<210> SEQ ID NO 86
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 86

tatactaaaa aagaattaag tcaagag 27

<210> SEQ ID NO 87
<211> LENGTH: 21
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 87

atggtagaaa sccccagcaa a 21

<210> SEQ ID NO 88
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: n is a, c, g or t

<400> SEQUENCE: 88

cacgtnttta gttactgcc a 20

<210> SEQ ID NO 89
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 89

gtactagtca gcgccactaa catcaa 26

<210> SEQ ID NO 90
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 90

gaagaatacg aaagcggcgg 20

<210> SEQ ID NO 91
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 91

tacttaggtc ttccgctttc gc 22

<210> SEQ ID NO 92
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 92

Thr Gly Thr Ala Ala Gly Ser Asp Val Asp Tyr Val Ser Lys Phe
1 5 10 15

<210> SEQ ID NO 93
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 93

Thr Arg Val Glu Trp Lys Ala Glu
1 5

<210> SEQ ID NO 94

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 94

Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys
1 5 10 15

<210> SEQ ID NO 95

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 95

Ser Trp Lys Cys Thr Gln Thr Gly
1 5

<210> SEQ ID NO 96

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 96

Ala Ala Lys Ala Glu Asp Leu Ser
1 5

<210> SEQ ID NO 97

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 97

Ala Thr Thr Asn Lys Thr Lys Glu Phe
1 5

<210> SEQ ID NO 98

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 98

Ala Val Gln Glu Lys Lys Pro Pro Glu Ala
1 5 10

<210> SEQ ID NO 99

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 99

ggctggggga gcagaag

17

<210> SEQ ID NO 100

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 100

Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp Tyr Val Ser Lys Phe
1 5 10 15

Gly Glu

<210> SEQ ID NO 101

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 101

Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp Tyr Val Ser Lys Phe
1 5 10 15

Gly Glu

<210> SEQ ID NO 102

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 102

Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp Tyr Val Ser Lys Phe
1 5 10 15

Gly Glu

<210> SEQ ID NO 103

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 103

Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp Tyr Val Ser Lys Phe
1 5 10 15

Gly Glu

<210> SEQ ID NO 104

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 104

Gly Thr Arg Val Glu Trp Lys Ala Glu
1 5

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<210> SEQ ID NO 105
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 105

Gly Thr Arg Val Glu Trp Lys Ala Glu
1 5

<210> SEQ ID NO 106
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 106

Gly Thr Arg Val Glu Trp Lys Ala Glu
1 5

<210> SEQ ID NO 107
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 107

Gly Thr Arg Val Glu Trp Lys Ala Glu
1 5

<210> SEQ ID NO 108
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 108

Lys Lys Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe Leu
1 5 10 15

Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu
20 25 30

Ala Val Gly Thr Ser Ala Lys Asp
35 40

<210> SEQ ID NO 109
<211> LENGTH: 41
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 109

Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe
1 5 10 15

Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala
20 25 30

Glu Ala Val Gly Thr Ser Ala Lys Asp
35 40

<210> SEQ ID NO 110
<211> LENGTH: 40

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 110

Lys Lys Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe Leu
1 5 10 15
Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu
20 25 30
Ala Val Gly Thr Ser Ala Lys Asp
35 40

<210> SEQ ID NO 111
<211> LENGTH: 41
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 111

Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe
1 5 10 15
Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala
20 25 30
Glu Ala Val Gly Thr Ser Ala Lys Asp
35 40

<210> SEQ ID NO 112
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 112

Ser Trp Lys Cys Thr Gln Thr Gly
1 5

<210> SEQ ID NO 113
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 113

Ser Trp Lys Cys Thr Gln Thr Gly
1 5

<210> SEQ ID NO 114
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 114

Ser Trp Lys Cys Thr Gln Thr Gly
1 5

<210> SEQ ID NO 115
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 115

Ser Trp Lys Cys Thr Gln Thr Gly
1 5

<210> SEQ ID NO 116
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 116

Ala Ala Lys Ala Glu Asp Leu Ser Ile Ala Leu Asn Arg Glu Leu Thr
1 5 10 15

Ser Ala Glu Lys Asn Lys
20

<210> SEQ ID NO 117
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 117

Ala Ala Lys Ala Glu Asp Leu Ser Ile Ala Leu Asn Arg Glu Leu Thr
1 5 10 15

Ser Ala Glu Lys Asn Lys
20

<210> SEQ ID NO 118
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 118

Ala Ala Lys Ala Glu Asp Leu Ser Thr Ala Leu Asn Arg Glu Leu Thr
1 5 10 15

Ser Ala Glu Lys Asn Lys
20

<210> SEQ ID NO 119
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 119

Ala Lys Ala Glu Asp Leu Ser Thr Ala Leu Asn Arg Glu Leu Thr Ser
1 5 10 15

Ala Glu Lys Asn Lys
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<210> SEQ ID NO 120
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 120

Ala Thr Thr Asn Lys Thr Lys Glu Phe
1 5

<210> SEQ ID NO 121

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 121

Ala Thr Thr Asn Lys Thr Lys Glu Phe
1 5

<210> SEQ ID NO 122

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 122

Ala Thr Thr Asn Lys Thr Lys Glu Phe
1 5

<210> SEQ ID NO 123

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 123

Ala Thr Thr Asn Lys Thr Lys Glu Phe
1 5

<210> SEQ ID NO 124

<211> LENGTH: 11

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 124

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11

<210> SEQ ID NO 125

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 125

gttggttatga tctgc

15

<210> SEQ ID NO 126

<211> LENGTH: 11

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 126

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ccttatgcat g 11

<210> SEQ ID NO 127
 <211> LENGTH: 14
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 127

cctcctaact tcct 14

<210> SEQ ID NO 128
 <211> LENGTH: 14
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 128

ttgttatgat ctgc 14

<210> SEQ ID NO 129
 <211> LENGTH: 14
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 129

gtaccttatg catg 14

<210> SEQ ID NO 130
 <211> LENGTH: 14
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 130

cctcctaact tcct 14

<210> SEQ ID NO 131
 <211> LENGTH: 17
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 131

aaggctgggt tgagtta 17

<210> SEQ ID NO 132
 <211> LENGTH: 14
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 132

ccctcttacc tctg 14

<210> SEQ ID NO 133
 <211> LENGTH: 183
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid
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<222> LOCATION: (177)..(178)
<223> OTHER INFORMATION: any amino acid
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<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (180)..(181)
<223> OTHER INFORMATION: any amino acid

<400> SEQUENCE: 133

Met Phe Met Thr Ser Gln Ala Gln Asn Gln Ser Ser Ile Pro Ile Thr
1             5             10             15

Val Glu Gly Lys Ala Arg Pro His Pro Val Asp Glu Tyr Val Gly Arg
20           25           30

Glu Ile Lys Lys Gln Arg Ile Met Lys Gly Met Ser Gln Asn Gln Leu
35           40           45

Ala Ser Arg Leu Gly Ile Thr Phe Gln Gln Val Gln Lys Tyr Glu Lys
50           55           60

Gly Thr Asn Arg Ile Val Ile Ser Arg Leu Tyr Glu Leu Ala Arg Val
65           70           75           80

Leu Gly Ile Glu Ile Asn Asp Leu Ile Ser Lys Leu Gln Asn Asp Leu
85           90           95

Arg Ser Ile Thr Glu Gly Thr Asp Xaa Ser Xaa Xaa Xaa Leu Xaa Glu
100          105          110

Gly Asp Glu Xaa Ser Leu Glu Glu Phe Xaa His Asn Tyr Asn Asp Gly
115          120          125

Lys Glu Val Leu Met Leu Val Arg Ala Tyr Arg Arg Ile Lys Ser Glu
130          135          140

Lys Met Arg Gly Ala Ile His Thr Leu Val Lys Val Met Cys Ala Glu
145          150          155          160

Gln Ser Asn Asp Asp Tyr Glu Xaa Ser Tyr Xaa Asp Xaa Glu Tyr Glu
165          170          175

Xaa Xaa Thr Xaa Xaa Glu Asp

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180

<210> SEQ ID NO 134
 <211> LENGTH: 185
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 134

Met Phe Met Thr Ser Gln Ala Gln Asn Gln Ser Ser Ile Pro Ile Thr
 1 5 10 15

Val Glu Gly Lys Val Arg Pro His Pro Val Asp Glu Tyr Val Gly Arg
 20 25 30

Glu Ile Lys Lys Gln Arg Ile Met Lys Gly Met Ser Gln Asn Gln Leu
 35 40 45

Ala Ser Arg Leu Gly Ile Thr Phe Gln Gln Val Gln Lys Tyr Glu Lys
 50 55 60

Gly Thr Asn Arg Ile Val Ile Ser Arg Leu Tyr Glu Leu Ala Arg Val
 65 70 75 80

Leu Gly Ile Glu Ile Asn Asp Leu Ile Ser Lys Leu Gln Asn Asp Leu
 85 90 95

Arg Ser Ile Thr Glu Gly Thr Asp Thr Ser Gly Thr Ser Phe Leu Lys
 100 105 110

Asp Gly Asp Glu Thr Ser Leu Glu Glu Phe Asn His Asn Tyr Asn Asp
 115 120 125

Gly Lys Glu Val Leu Met Leu Val Arg Ala Tyr Arg Lys Ile Lys Ser
 130 135 140

Glu Lys Met Arg Gly Ala Ile His Thr Leu Val Lys Val Met Cys Ala
 145 150 155 160

Glu Gln Ser Ser Asn Asp Asp Tyr Glu Asn Ser Tyr Val Asp Ser Asp
 165 170 175

Tyr Glu Ser Gly Thr Gly Thr Glu Asp
 180 185

<210> SEQ ID NO 135
 <211> LENGTH: 183
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 135

Met Phe Met Thr Ser Gln Ala Gln Asn Gln Asn Ser Ile Pro Ile Thr
 1 5 10 15

Ile Glu Gly Lys Ala Lys Pro His Pro Val Asp Glu Tyr Val Gly Arg
 20 25 30

Glu Ile Lys Lys Gln Arg Ile Met Lys Gly Met Ser Gln Asn Gln Leu
 35 40 45

Ala Ser Arg Leu Gly Ile Thr Phe Gln Gln Val Gln Lys Tyr Glu Lys
 50 55 60

Gly Thr Asn Arg Ile Val Ile Ser Arg Leu Tyr Glu Leu Ala Arg Val
 65 70 75 80

Leu Gly Ile Glu Ile Asn Asp Leu Met Ser Lys Leu Gln Asn Asp Ile
 85 90 95

Arg Ser Ile Thr Glu Gly Thr Asp Ile Ser Ile Thr Cys Leu Gln Glu
 100 105 110

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Gly Asp Glu Ala Ser Leu Glu Glu Phe Asp His Asn Tyr Asn Asp Gly
 115 120 125

Lys Glu Val Leu Met Leu Val Arg Ala Tyr Arg Arg Ile Lys Ser Glu
 130 135 140

Lys Met Arg Gly Ala Ile His Thr Leu Val Lys Val Met Cys Ala Glu
 145 150 155 160

Gln Ser Asn Asp Asp Tyr Glu Thr Ser Tyr Arg Gly Pro Glu Tyr Val
 165 170 175

Ile Val Thr Asn Gln Glu Asp
 180

<210> SEQ ID NO 136
 <211> LENGTH: 185
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 136

Met Thr Ser Arg Thr Gln Asn Gln Ser Ser Ile Pro Ile Ile Val Glu
 1 5 10 15

Gly Lys Ala Arg Pro His Pro Val Asp Glu Tyr Val Gly Arg Glu Ile
 20 25 30

Lys Lys Gln Arg Ile Met Lys Gly Met Ser Gln Asn Gln Leu Ala Ser
 35 40 45

Arg Leu Gly Ile Thr Phe Gln Gln Val Gln Lys Tyr Glu Lys Gly Thr
 50 55 60

Asn Arg Ile Val Ile Ser Arg Leu Tyr Glu Leu Ala Arg Val Leu Gly
 65 70 75 80

Ile Glu Ile Lys Asp Leu Ile Ala Lys Leu Gln Asn Asp Leu Arg Pro
 85 90 95

Ile Thr Asp Ala Gly Asp Ala Thr Asp Ala Ala Leu Arg Glu Gly Glu
 100 105 110

Glu Ser Ser Leu Glu Glu Phe Gly Gln Ser Tyr Asn Asp Gly Lys Glu
 115 120 125

Val Leu Met Leu Val Arg Ala Tyr Arg Arg Ile Lys Ser Asp Lys Met
 130 135 140

Arg Gly Ala Ile His Thr Leu Val Lys Val Met Cys Ala Glu Gln Gln
 145 150 155 160

Gln Asp Asp Tyr Glu His Ser Asp Ala Asp Glu Glu Leu Gly Tyr Glu
 165 170 175

His Asp Pro Glu Ser Glu Thr Gly Ala
 180 185

<210> SEQ ID NO 137
 <211> LENGTH: 326
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: any amino acid
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 <222> LOCATION: (6)..(6)
 <223> OTHER INFORMATION: any amino acid
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 <222> LOCATION: (10)..(10)

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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid
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<222> LOCATION: (112)..(112)
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid

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<220> FEATURE:
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<222> LOCATION: (310)..(310)
<223> OTHER INFORMATION: any amino acid
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<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (314)..(314)
<223> OTHER INFORMATION: any amino acid

<400> SEQUENCE: 137

Met Lys Lys Xaa Ile Xaa Val Phe Ala Xaa Ala Xaa Xaa Met Leu Xaa
1          5          10          15

Leu Pro Ser Xaa Ser Phe Ala Ser Pro Xaa Pro Val Asp Phe Ser Arg
20          25          30

Xaa Glu Gly Ala Ser Gly Phe Phe Ala Ser Val Gln Tyr Lys Tyr Ala
35          40          45

Val Pro Tyr Phe Gly Xaa Phe Xaa Leu Glu Xaa Gly Gly Lys Xaa Leu
50          55          60

Asn Xaa Phe Ser Ala Xaa Xaa Glu Lys Lys Xaa Xaa Glu Xaa Xaa Xaa
65          70          75          80

Ala Xaa Ala Xaa Ala Xaa Xaa Xaa Xaa Ala Ala Pro Ser Xaa Xaa Glu
85          90          95

Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Phe Gln Gly Lys Tyr Ser Pro Xaa
100         105         110

Tyr Leu Xaa Ser Ala Xaa Ala Xaa Ser Xaa Ser Ala Gly Tyr Ser Thr
115         120         125

Gly Xaa Val Arg Xaa Glu Ala Glu Gly Met Xaa Gln Lys Phe Xaa Val
130         135         140

Asp Xaa Lys Lys Tyr Lys Xaa Xaa Xaa Xaa Ala Xaa Ala Tyr Arg Phe
145         150         155         160

Ala Ala Ser Ala Pro Ser Glu Asn Xaa Xaa Xaa Pro Xaa Ala Thr Xaa
165         170         175

Pro Xaa Glu Lys Tyr Xaa Ile Thr Leu Glu Asn Arg Asp Val Xaa Ile
180         185         190

Thr Ser Leu Val Ala Asn Leu Cys Tyr Asp Met Xaa Pro Glu Xaa Ser
195         200         205

Xaa Ile Ser Pro Ser Ala Cys Val Gly Xaa Gly Xaa Ser Xaa Val Lys
210         215         220

Xaa Leu Gly Val Leu Glu Gln Arg Trp Ala Tyr Gln Ala Lys Val Gly
225         230         235         240

Val Gln Tyr Phe Xaa Ser Arg Lys Ala Xaa Xaa Phe Leu Ser Ala Tyr
245         250         255

Val Ser Xaa Val Xaa Gly Glu Lys Phe Xaa Asn Val Xaa Val Lys His
260         265         270

Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Ser Xaa Gly Ala Xaa Gly Ser Gly
275         280         285

Xaa Gly Xaa Xaa Ser Xaa Ser Xaa Ala Xaa Xaa Xaa Xaa Xaa Leu
290         295         300

Leu Tyr Pro Asp Ala Xaa Leu Ser Leu Xaa Tyr Tyr Gly Phe Glu Cys
305         310         315         320

Gly Val Arg Leu Val Leu
325

<210> SEQ ID NO 138
<211> LENGTH: 306
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 138

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Met Lys Lys Lys Ile Cys Val Phe Ala Leu Pro Thr Val Met Phe Met
1      5      10      15
Leu Pro Ser Leu Ser Phe Ala Ser Pro Lys Pro Val Asp Phe Ser Arg
      20      25      30
Gln Ala Gly Ile Glu Gly Phe Phe Ser Ser Ile Gln Tyr Lys Tyr Ala
      35      40      45
Val Pro Tyr Phe Gly Ala Phe Ser Leu Val His Gly Gly Asn Pro Leu
      50      55      60
Asp Val Phe Ser Ala Lys Asp Ala Glu Ser Ser Ser Gly Ile Ala Thr
      65      70      75      80
Leu Leu Gln Ser Val Ala Ser Thr Ser Thr Ser Asp Ala Glu Asn Phe
      85      90      95
Gln Gly Lys Tyr Asn Pro Ser Tyr Leu His Ser Lys Gln Ala Leu Ser
      100     105     110
Ala Ser Ala Gly Tyr Ser Thr Gly Tyr Val Arg Val Glu Val Glu Gly
      115     120     125
Met His Gln Lys Phe Leu Val Asp Pro Lys Arg Tyr Lys Glu Arg Asp
      130     135     140
Lys Ala Lys Ala Tyr Arg Phe Ala Ala Ser Ala Ser Ser Gly Gly Thr
      145     150     155     160
Gly Gln Pro Thr Ala Thr His Pro Asn Glu Lys Tyr Tyr Ile Ser Leu
      165     170     175
Glu Asn Arg Asp Leu Ile Ile Thr Ser Leu Val Ala Asn Leu Cys Tyr
      180     185     190
Asp Met Ile Pro Glu Glu Ser Arg Leu Ser Pro Asn Ile Cys Val Gly
      195     200     205
Ala Gly Ile Gly Tyr Val Lys Ala Phe Gly Val Leu Glu Gln Arg Trp
      210     215     220
Ala Tyr Gln Ala Lys Val Gly Val Gln Tyr Phe Leu Ser Arg Lys Ala
      225     230     235     240
Ser Val Phe Leu Ser Ala Tyr Val Asp Lys Val Asn Gly Glu Lys Phe
      245     250     255
Lys Asn Val Arg Val Lys His Asn Ile Gly Thr Arg Ser Ser Ser Ser
      260     265     270
Gly Gly Thr Ser Gln Ser Ile Ser Thr Asp Ser Ile Leu Tyr Pro Asp
      275     280     285
Ala His Leu Ser Leu Leu Tyr Tyr Gly Leu Glu Cys Gly Val Arg Leu
      290     295     300
Thr Leu
305

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<210> SEQ ID NO 139

<211> LENGTH: 330

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 139

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Met Lys Lys Val Tyr Gly Leu Val Tyr Ala Ala Leu Ser Leu Leu Phe
1      5      10      15
Thr Pro Cys Gly Ser Phe Ala Ser Pro Arg Pro Ile Asp Phe Ser Arg

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-continued

20					25					30					
Gly	Glu	Gly	Ala	Ser	Gly	Phe	Phe	Ala	Ser	Val	Gln	Tyr	Lys	Leu	Ala
	35					40					45				
Val	Pro	His	Phe	Arg	Asp	Phe	Ile	Val	Glu	Asp	Lys	Gly	Lys	Ala	Leu
	50					55					60				
Asn	Thr	Phe	Ala	Met	Lys	Glu	Lys	Gln	Gln	Gly	Gly	Thr	Ala	Lys	Ala
	65					70					75				80
Ala	Ala	Gly	Ala	Ala	Thr	Pro	Pro	Ala	Ala	Pro	Ser	Gly	Ala	Glu	Ala
			85					90						95	
Pro	Pro	Ala	Lys	Gly	Pro	Asp	Leu	Ala	Ser	Gly	Gly	Ser	Phe	Glu	Gly
		100					105						110		
Lys	Tyr	Ser	Pro	Glu	Tyr	Leu	Arg	Ser	Ala	Lys	Ala	Gly	Ser	Val	Ser
	115					120						125			
Val	Gly	Tyr	Ser	Ala	Gly	Asn	Val	Arg	Leu	Glu	Ala	Glu	Gly	Met	Tyr
	130					135					140				
Gln	Lys	Phe	Pro	Val	Asp	Thr	Lys	Lys	Tyr	Lys	Asp	Asn	Pro	Glu	Arg
	145					150					155				160
Ala	Tyr	Arg	Phe	Ala	Ile	Ser	Ala	Pro	Asp	Glu	Asn	Ser	Thr	Thr	Val
			165					170						175	
Ala	Thr	Arg	Pro	Gln	Glu	Pro	Tyr	His	Ile	Thr	Ala	Glu	Asn	Lys	Glu
			180					185					190		
Val	Thr	Thr	Ala	Ser	Leu	Met	Ala	Asn	Leu	Cys	Tyr	Asp	Leu	Leu	Pro
		195					200					205			
Glu	Ser	Ser	Gln	Ile	Ser	Pro	Ser	Ala	Cys	Val	Gly	Gly	Gly	Gly	Ser
	210					215					220				
Leu	Val	Arg	Phe	Leu	Gly	Val	Thr	Glu	Val	Arg	Trp	Ala	Tyr	Gln	Ala
	225					230					235				240
Lys	Val	Gly	Val	Gln	Tyr	Phe	Ala	Ser	Arg	Lys	Ala	Ala	Leu	Phe	Ala
			245					250						255	
Tyr	Ala	Tyr	Ala	Ser	Arg	Val	His	Pro	Glu	Lys	Phe	Ser	Asn	Ile	Pro
		260						265					270		
Val	Val	His	His	Ile	Lys	Thr	Glu	Ser	Pro	Lys	Gly	Ser	Gln	Gly	Ala
		275					280					285			
Ala	Gly	Ser	Gly	Gly	Gly	Glu	Ser	Ser	Ala	Gln	Ala	Ala	Gly	Gly	Lys
	290					295					300				
Leu	Pro	Gly	Leu	Leu	Tyr	Pro	Gln	Ala	Ser	Leu	Gly	Leu	Asp	Tyr	Phe
	305					310					315				320
Gly	Phe	Glu	Cys	Gly	Ile	Arg	Leu	Val	Leu						
			325					330							

<210> SEQ ID NO 140

<211> LENGTH: 418

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(3)

<223> OTHER INFORMATION: any amino acid

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (5)..(10)

<223> OTHER INFORMATION: any amino acid

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<222> LOCATION: (12)..(14)

<223> OTHER INFORMATION: any amino acid

<220> FEATURE:

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<223> OTHER INFORMATION: any amino acid

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<222> LOCATION: (248)..(248)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (251)..(251)

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<223> OTHER INFORMATION: any amino acid
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<223> OTHER INFORMATION: any amino acid
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<222> LOCATION: (412)..(412)
<223> OTHER INFORMATION: any amino acid

<400> SEQUENCE: 140

Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Met Xaa Xaa Xaa Lys Xaa
1 5 10 15

Ala Leu Xaa Xaa Ala Val Ala Met Xaa Xaa Xaa Xaa Ala Gly
20 25 30

Xaa Xaa Xaa Ala Ala Xaa Xaa Asp Val Xaa Xaa Xaa Ser Xaa Xaa Gly

-continued

35					40					45					
Ala	Gly	Ser	Phe	Tyr	Val	Gly	Leu	Asp	Tyr	Ser	Pro	Ala	Phe	Ser	Lys
50						55					60				
Ile	Xaa	Asp	Phe	Xaa	Ile	Arg	Glu	Ser	Xaa	Gly	Glu	Thr	Xaa	Ala	Val
65					70					75					80
Tyr	Pro	Tyr	Xaa	Lys	Asp	Gly	Xaa	Arg	Val	Xaa	Xaa	Lys	Xaa	His	Lys
				85					90					95	
Phe	Asp	Trp	Asn	Thr	Pro	Asp	Pro	Arg	Ile	Xaa	Phe	Lys	Asp	Asn	Met
			100					105					110		
Leu	Val	Ala	Leu	Glu	Gly	Ser	Val	Gly	Tyr	Ser	Ile	Gly	Gly	Ala	Arg
		115					120					125			
Val	Glu	Leu	Glu	Ile	Gly	Tyr	Glu	Arg	Phe	Lys	Thr	Lys	Gly	Ile	Arg
	130						135					140			
Asp	Ser	Gly	Ser	Lys	Glu	Glu	Glu	Ala	Asp	Xaa	Val	Tyr	Leu	Leu	Ala
145				150					155						160
Lys	Glu	Leu	Ala	Tyr	Asp	Xaa	Val	Xaa	Gly	Gln	Xaa	Asp	Xaa	Leu	Ala
			165						170					175	
Xaa	Ala	Leu	Xaa	Lys	Thr	Xaa	Xaa	Xaa	Glu	Ile	Val	Lys	Phe	Ala	Xaa
		180						185					190		
Ala	Val	Glu	Xaa	Ser	Xaa	Xaa	Gly	Ile	Xaa	Xaa	Lys	Val	Cys	Lys	Xaa
		195					200					205			
Xaa	Gly	Ser	Xaa	Xaa	Xaa	Ala	Gly	Xaa	Xaa	Lys	Cys	Gly	Xaa	Gln	Xaa
	210						215					220			
Xaa	Ser	Asp	Xaa	Xaa	Xaa	Thr	Xaa	Glu	Xaa	Ser	Xaa	Xaa	Phe	Thr	Xaa
225				230					235						240
Xaa	Xaa	Xaa	Asn	Thr	Leu	Ser	Xaa	Gly	Lys	Xaa	Trp	Pro	Xaa	Xaa	Xaa
			245						250				255		
Asn	Xaa	Xaa	Xaa	Asn	Ala	Xaa	Xaa	Xaa	Ala	Xaa	Xaa	Leu	Asn	Xaa	Xaa
		260						265					270		
Leu	Thr	Xaa	Xaa	Glu	Lys	Xaa	Ile	Val	Ala	Gly	Leu	Leu	Ala	Arg	Thr
	275						280					285			
Ile	Glu	Gly	Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val	Ser	Ser	Thr	Ser
	290						295					300			
Val	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Leu	Leu	Ser	Glu	Gly	Xaa	Gly	Val
305				310						315					320
Val	Pro	Tyr	Ala	Cys	Xaa	Gly	Xaa	Gly	Gly	Asn	Phe	Val	Gly	Val	Val
			325						330				335		
Asp	Gly	His	Ile	Thr	Pro	Lys	Leu	Ala	Tyr	Arg	Val	Lys	Ala	Gly	Leu
		340						345					350		
Ser	Tyr	Xaa	Leu	Ser	Pro	Glu	Ile	Ser	Ala	Phe	Ala	Gly	Gly	Phe	Tyr
	355						360					365			
His	Arg	Val	Leu	Gly	Asp	Gly	Xaa	Tyr	Asp	Asp	Leu	Pro	Xaa	Gln	Arg
	370						375					380			
Leu	Val	Asp	Asp	Thr	Xaa	Thr	Ala	Gly	Lys	Thr	Lys	Asp	Thr	Ala	Ile
385				390					395						400
Ala	Ser	Phe	Xaa	Met	Ala	Tyr	Xaa	Gly	Gly	Glu	Xaa	Gly	Val	Arg	Phe
			405						410					415	

Ala Phe

<210> SEQ ID NO 141

<211> LENGTH: 407

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 141

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Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
 1           5           10           15

Ala Leu Val Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
 20           25           30

Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
 35           40           45

Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
 50           55           60

Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
 65           70           75           80

Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
 85           90           95

Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
100          105          110

Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
115          120          125

Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
130          135          140

Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
145          150          155          160

Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Thr Ala
165          170          175

Leu Gly Lys Met Thr Lys Gly Glu Ala Lys Lys Trp Gly Asn Ala Val
180          185          190

Glu Asn Ala Thr Asn Gly Asp Lys Val Ser Gln Asn Val Cys Lys Gly
195          200          205

Thr Gly Ser Thr Gly Ser Ser Gly Asn Lys Cys Gly Thr Thr Asp Ser
210          215          220

Thr Ala Thr Thr Lys Ile Ser Ala Val Phe Thr Glu Asp Ala Ala Ala
225          230          235          240

Gln Leu Ser Thr Met Asp Asn Thr Thr Ile Asn Thr Thr Gly Met Ala
245          250          255

Asn Asn Ile Asn Ser Leu Thr Lys Asp Glu Lys Ala Ile Val Ala Gly
260          265          270

Ala Phe Ala Arg Ala Val Glu Gly Ala Glu Val Ile Glu Val Arg Ala
275          280          285

Ile Gly Ser Thr Ser Val Met Leu Asn Ala Cys Tyr Asp Leu Leu Thr
290          295          300

Asp Gly Ile Gly Val Val Pro Tyr Ala Cys Ala Gly Ile Gly Gly Asn
305          310          315          320

Phe Val Ser Val Val Asp Gly His Ile Asn Pro Lys Phe Ala Tyr Arg
325          330          335

Val Lys Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu Ile Ser Ala Phe
340          345          350

Ala Gly Ala Phe Tyr His Lys Val Leu Gly Asp Gly Asp Tyr Asp Glu
355          360          365

Leu Pro Leu Ser His Ile Ser Asp Tyr Thr Gly Thr Ala Gly Lys Asn
370          375          380

Lys Asp Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe Gly Gly Glu
385          390          395          400

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Leu Gly Val Arg Phe Ala Phe
405

<210> SEQ ID NO 142
 <211> LENGTH: 431
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 142

Met Arg Lys Gly Lys Ile Ile Leu Gly Ser Val Met Met Ser Met Ala
 1 5 10 15
 Ile Val Met Ala Gly Asn Asp Val Arg Ala His Asp Asp Val Ser Ala
 20 25 30
 Leu Glu Thr Gly Gly Ala Gly Tyr Phe Tyr Val Gly Leu Asp Tyr Ser
 35 40 45
 Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile Arg Glu Ser Asn Gly
 50 55 60
 Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp Gly Lys Ser Val Lys
 65 70 75 80
 Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile Gly
 85 90 95
 Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly Ser Val Gly Tyr Gly
 100 105 110
 Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Arg Phe Lys
 115 120 125
 Thr Lys Gly Ile Arg Asp Ser Gly Ser Lys Glu Asp Glu Ala Asp Thr
 130 135 140
 Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp Val Val Thr Gly Gln
 145 150 155 160
 Thr Asp Asn Leu Ala Ala Ala Leu Ala Lys Thr Ser Gly Lys Asp Ile
 165 170 175
 Val Gln Phe Ala Lys Ala Val Glu Ile Ser Asn Ser Gly Ile Gly Lys
 180 185 190
 Lys Val Cys Glu Thr Lys Arg Lys Asp Gly Asp Thr Thr Asn Arg Phe
 195 200 205
 Ala Lys Tyr Ile Val Gly Ala Gly Asp Ser Ser Asn Ala Gly Thr Ser
 210 215 220
 Leu Cys Gly Gly Lys Asn Gln Lys Ser Ser Asp Thr Asp Thr Gly Val
 225 230 235 240
 Glu Lys Ala Gln Ala Leu His Asp Phe Val Ser Asn Thr Leu Ser Asp
 245 250 255
 Gly Thr Lys Asn Trp Pro Thr Ser Ser Glu Thr Ser Lys Ser Asn Asn
 260 265 270
 Asp Asn Ala Lys Ala Val Ala Gly Asp Leu Thr Lys Lys Leu Thr Pro
 275 280 285
 Glu Glu Lys Thr Ile Val Ala Gly Leu Leu Ala Lys Thr Ile Glu Gly
 290 295 300
 Gly Glu Val Val Glu Ile Arg Ala Val Ser Ser Thr Ser Val Met Val
 305 310 315 320
 Asn Ala Cys Tyr Asp Leu Leu Ser Glu Gly Leu Gly Val Val Pro Tyr
 325 330 335
 Ala Cys Val Gly Leu Gly Gly Asn Phe Val Gly Val Val Asp Gly His
 340 345 350

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Ile Thr Pro Lys Leu Ala Tyr Arg Leu Lys Ala Gly Leu Ser Tyr Gln
    355                      360                      365

Leu Ser Pro Glu Ile Ser Ala Phe Ala Gly Gly Phe Tyr His Arg Val
    370                      375                      380

Val Gly Asp Gly Val Tyr Asp Asp Leu Pro Ala Gln Arg Leu Val Asp
    385                      390                      395                      400

Asp Thr Ser Pro Ala Gly Arg Thr Lys Asp Thr Ala Ile Ala Asn Phe
    405                      410                      415

Ser Met Ala Tyr Val Gly Gly Glu Phe Gly Val Arg Phe Ala Phe
    420                      425                      430

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<210> SEQ ID NO 143
<211> LENGTH: 458
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 143

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Met Leu Cys Leu Leu Val Val Glu Leu Trp Asn Val Lys Leu Val Ser
 1                      5                      10                      15

Val Gly Glu Ser Thr Gly Glu Ser Arg Asn Thr Val Glu Val Cys Cys
                20                      25                      30

Ala Arg Glu Lys Gly Val Arg Arg Arg Glu Ala Ile Val Lys Gly Ser
    35                      40                      45

Glu Val Lys Gly Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val
    50                      55                      60

Ala Met Thr Val Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly
 65                      70                      75                      80

Ser Asp Val Asp Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val
    85                      90                      95

Gly Leu Asn Tyr Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile
    100                      105                      110

Arg Glu Ser Thr Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp
    115                      120                      125

Gly Thr Arg Val Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro
    130                      135                      140

Asp Pro Arg Ile Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly
 145                      150                      155                      160

Ser Val Gly Tyr Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly
    165                      170                      175

Tyr Glu Gln Phe Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu
    180                      185                      190

Glu Glu Ala Asp Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr
    195                      200                      205

Leu Val Ser Asp Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr
    210                      215                      220

Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala
 225                      230                      235                      240

Lys Asp Ile Asp Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala
    245                      250                      255

Ala Gly Ser Trp Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr
    260                      265                      270

Ala Glu Phe Ser Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn
    275                      280                      285

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Lys Gly Lys Ala Trp Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu
 290 295 300
 Asp Leu Ser Ile Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn
 305 310 315 320
 Lys Val Ala Gly Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val
 325 330 335
 Glu Ile Arg Ala Val Ser Thr Thr Ser Val Met Leu Asn Gly Cys Tyr
 340 345 350
 Asp Leu Gln Ser Glu Gly Phe Ser Ile Val Pro Tyr Ala Cys Leu Gly
 355 360 365
 Val Gly Ala Asn Phe Val Gly Ile Val Asp Gly His Val Thr Pro Lys
 370 375 380
 Leu Ala Tyr Lys Val Lys Ala Gly Leu Ser Tyr Glu Leu Ser Pro Glu
 385 390 395 400
 Ile Ser Met Phe Ala Gly Gly Phe Tyr His Arg Val Leu Gly Glu Gly
 405 410 415
 Glu Tyr Asp Asp Leu Pro Val Gln Arg Leu Val Asp Asp Ala Thr Thr
 420 425 430
 Asn Lys Thr Lys Glu Phe Ala Lys Ala Ser Phe Lys Met Ala Tyr Thr
 435 440 445
 Gly Ala Glu Ile Gly Val Arg Ser Ala Phe
 450 455

<210> SEQ ID NO 144
 <211> LENGTH: 36
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 144

Asn Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala
 1 5 10 15
 Ala Asp Glu Ala Ala Glu Pro Ala Thr Pro Ala Pro Ser Ser Pro Glu
 20 25 30
 Gly Phe Gly Ser
 35

<210> SEQ ID NO 145
 <211> LENGTH: 22
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 145

Glu Asn Thr Glu Lys Glu Leu Thr Leu Phe Thr Leu Lys Glu Ser Thr
 1 5 10 15
 Asp Thr Pro Thr Phe Lys
 20

<210> SEQ ID NO 146
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 146

Asp Val Phe Ser Ala Lys Asp Ala Glu Ser Ser Ser Gly Ile Ala Thr

-continued

1 5 10 15
 Leu Leu Gln Ser Val Ala Ser Thr Ser Thr Ser
 20 25

<210> SEQ ID NO 147
 <211> LENGTH: 22
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 147

Glu Lys Ser Glu Lys Glu Leu Thr Leu Phe Ser Leu Lys Glu Glu Thr
 1 5 10 15

Glu Thr Ile Asp Leu Lys
 20

<210> SEQ ID NO 148
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 148

Lys Gln Asp Lys Glu Leu Thr Leu Phe Ser Leu Lys Glu Glu Asn Thr
 1 5 10 15

Glu Leu Lys Leu Asn
 20

<210> SEQ ID NO 149
 <211> LENGTH: 37
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 149

Asn Thr Phe Ala Met Lys Glu Lys Gln Gln Gly Gly Thr Ala Lys Ala
 1 5 10 15

Ala Ala Gly Ala Ala Thr Pro Pro Ala Ala Pro Ser Gly Ala Glu Ala
 20 25 30

Pro Pro Ala Lys Gly
 35

<210> SEQ ID NO 150
 <211> LENGTH: 25
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 150

Ser Glu Ala Asp Lys Ser Glu Lys Glu Leu Thr Leu Phe Thr Leu Lys
 1 5 10 15

Glu Ser Thr Gln Ala Pro Asp Phe Thr
 20 25

<210> SEQ ID NO 151
 <211> LENGTH: 41
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 151

Pro Tyr Phe Gly Ser Leu Thr Leu Glu Ser Gly Gly Lys Thr Leu Asn
 1 5 10 15

Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala Ala
 20 25 30

Asp Glu Ala Ala Glu Pro Ala Thr Pro
 35 40

<210> SEQ ID NO 152

<211> LENGTH: 32

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 152

Pro Tyr Phe Gly Ala Phe Ser Leu Val His Gly Gly Asn Pro Leu Asp
 1 5 10 15

Val Phe Ser Ala Lys Asp Ala Glu Ser Ser Ser Gly Ile Ala Thr Leu
 20 25 30

<210> SEQ ID NO 153

<211> LENGTH: 38

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 153

Pro His Phe Arg Asp Phe Ile Val Glu Asp Lys Gly Lys Ala Leu Asn
 1 5 10 15

Thr Phe Ala Met Lys Glu Lys Gln Gln Gly Gly Thr Ala Lys Ala Ala
 20 25 30

Ala Gly Ala Ala Thr Pro
 35

<210> SEQ ID NO 154

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 154

Pro Arg Phe Ser Pro Ile Ser Ala Lys Tyr Lys Thr Asp Glu Lys Ser
 1 5 10 15

Glu Lys Glu Leu Thr Leu
 20

<210> SEQ ID NO 155

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 155

Pro Arg Phe Ser Pro Ile Ser Val Lys Tyr Lys Thr Asp Glu Asn Thr
 1 5 10 15

Glu Lys Glu Leu Thr Leu
 20

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<210> SEQ ID NO 156
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 156

Pro Met Phe Ser Pro Ile Ser Val Lys Tyr Lys Ser Thr Gly Asn Ser
 1 5 10 15

Glu Ala Asp Lys Ser Glu Lys Glu Leu Thr Leu
 20 25

<210> SEQ ID NO 157
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 157

Pro Lys Phe Ser Ala Ile Ser Ala Lys Tyr Lys His Glu Lys Gln Asp
 1 5 10 15

Lys Glu Leu Thr Leu
 20

<210> SEQ ID NO 158
 <211> LENGTH: 273
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 158

accgtcttgc cactgcttta ggtaagatga ctaagggtga agctaagaag tggggtaatg	60
ccatagagag tgctactggc actactagtgt gtgatgaact gagtaagaag gtgtgtggca	120
agggtaccac tagtggtagc accaaccagt gtggtaccac cgatagcact gccaccacca	180
agattagtga ggtgttcact gagggtagac acacactgct ttctgttgag gggaacaaag	240
acaccaccaa cttgcagggg atggcggaata aca	273

<210> SEQ ID NO 159
 <211> LENGTH: 359
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 159

ataaccttgc cgctgctctt gccaaaacct caggtaagga catcggtcag ttgctaagg	60
ccgtggagat ttctaattcc ggtatttgta agaagggtgtg tgagacaaag cggaaggatg	120
gtgatactac gaacagggtt gcaaagtata tagttggtgc ggggtgatagt agcaatgctg	180
gtacatcatt gtgtggtggt aagaacaaa agagttcggc cacagacacc ggggtggaga	240
aggctcaggc tctgcatgac tttgtttcta acacattgag tgatgggtact aagaactggc	300
ctacgtcgag tgaacgtctt aaatcgaata acgacaacgc caaagctgta gcgggagac	359

<210> SEQ ID NO 160
 <211> LENGTH: 284
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 160

ataaattcct ggaggagctg aagaatacga aagcggcgga gatcggtaaa ttgctgagg      60
ctgttgccac atcggaag gatattgatg gaaaggtttg taagaagggc ggcagcgga      120
atgccgcggg cagctggaag tgtacgcaga ctggcagcaa cggcgctcagc accgcagagt      180
tcagtaaaat atttacgaag gcagacgtaa atactgacaa caaaggcaaa gcatggccta      240
acgggaacaa cgacgctgcg aaagcggaag acctaagtat tgcg                        284

<210> SEQ ID NO 161
<211> LENGTH: 292
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (22)..(23)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (34)..(34)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (37)..(37)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (41)..(41)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(65)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (70)..(70)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(79)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (98)..(98)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (113)..(113)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (116)..(117)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (132)..(132)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (136)..(136)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (140)..(140)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (143)..(143)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (147)..(147)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (152)..(152)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (155)..(155)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (160)..(160)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (180)..(180)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (183)..(183)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (194)..(194)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (201)..(201)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (203)..(203)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (210)..(210)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (218)..(218)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (219)..(219)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (221)..(221)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (226)..(227)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (230)..(230)
<223> OTHER INFORMATION: a, c, g or t

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (238)..(238)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (245)..(247)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (258)..(259)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (261)..(261)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (263)..(263)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (269)..(269)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (278)..(278)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (281)..(282)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (288)..(288)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (290)..(290)
<223> OTHER INFORMATION: a, c, g or t

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<400> SEQUENCE: 161

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ataaacttgc cgctgctctn gnaaanacga cagngggnga natcgtaag ttgctaagg      60
ccgtngagan ttctactnnc gntattggtg gnaaggtntg tgagaaaagc ggnagnntgg    120
caatgctacg ancagntggn agngtanaca gntgnggtgn cagcaacagc gctggcaccn    180
canagtttag tganaagatc nangagggtn cagacacana nactgnngtn gagaaggnc      240
aagcnnngcc taacttgnc nangacacng cgagtganag nnctaagnan tg              292

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<210> SEQ ID NO 162
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(4)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(7)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (22)..(22)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (172)..(172)

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<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (184)..(185)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (194)..(195)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (203)..(203)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (210)..(210)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (213)..(213)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (220)..(220)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (229)..(229)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (238)..(238)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (239)..(239)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (240)..(240)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (248)..(248)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (250)..(250)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (371)..(371)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (389)..(389)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (391)..(391)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (409)..(409)
<223> OTHER INFORMATION: any amino acid

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<400> SEQUENCE: 162

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Xaa Xaa Xaa Xaa Lys Xaa Xaa Leu Gly Xaa Val Met Met Ser Leu Ala
1           5           10           15

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Ile Val Met Ala Gly Xaa Asp Val Arg Ala His Asp Asp Val Ser Ala
                20           25           30

```

```

Leu Gly Thr Gly Gly Ala Gly Ser Phe Tyr Val Gly Leu Asp Tyr Ser
35           40           45

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Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile Arg Glu Ser Asn Gly
50           55           60

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Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp Gly Lys Arg Val Lys
 65 70 75 80
 Leu Lys Ser His Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile Gly
 85 90 95
 Phe Lys Asp Asn Met Leu Val Ala Leu Glu Gly Ser Val Gly Tyr Ser
 100 105 110
 Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Arg Phe Lys
 115 120 125
 Thr Lys Gly Ile Arg Asp Ser Gly Ser Lys Glu Glu Glu Ala Asp Thr
 130 135 140
 Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp Val Val Thr Gly Gln
 145 150 155 160
 Thr Asp Lys Leu Ala Ala Ala Leu Ala Lys Thr Xaa Gly Lys Glu Ile
 165 170 175
 Val Lys Phe Ala Asn Ala Val Xaa Xaa Ser Ala Lys Asp Ile Asp Lys
 180 185 190
 Lys Val Cys Lys Lys Gly Thr Gly Asn Thr Xaa Ser Ser Trp Lys Cys
 195 200 205
 Gly Xaa Thr Gly Ser Thr Ala Thr Thr Lys Lys Phe Ser Ala Phe Phe
 210 215 220
 Thr Lys Ala Val Xaa Glu Gly Lys Asn Trp Pro Thr Gly Xaa Asn Xaa
 225 230 235 240
 Asn Ala Asn Ala Glu Asp Met Ala Thr Asp Leu Asn Glu Leu Thr Lys
 245 250 255
 Glu Glu Lys Thr Ile Val Ala Gly Leu Leu Ala Arg Thr Ile Glu Gly
 260 265 270
 Gly Glu Val Val Glu Ile Arg Ala Val Ser Ser Thr Ser Val Met Leu
 275 280 285
 Asn Ala Cys Tyr Asp Leu Leu Ser Glu Gly Leu Gly Val Val Pro Tyr
 290 295 300
 Ala Cys Val Gly Leu Gly Gly Asn Phe Val Gly Val Val Asp Gly His
 305 310 315 320
 Ile Thr Pro Lys Leu Ala Tyr Arg Val Lys Ala Gly Leu Ser Tyr Gln
 325 330 335
 Leu Ser Pro Glu Ile Ser Ala Phe Ala Gly Gly Phe Tyr His Arg Val
 340 345 350
 Leu Gly Asp Gly Val Tyr Asp Asp Leu Pro Leu Gln Arg Leu Val Asp
 355 360 365
 Asp Thr Xaa Thr Ala Gly Lys Thr Lys Asp Thr Ala Ile Ala Ser Phe
 370 375 380
 Ser Met Ala Tyr Xaa Gly Gly Glu Phe Gly Val Arg Phe Ala Phe
 385 390 395

<210> SEQ ID NO 163

<211> LENGTH: 80

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 163

Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile
 1 5 10 15
 Asp Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala Ala Gly Ser
 20 25 30

-continued

Trp Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr Ala Glu Phe
35 40 45

Ser Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys
50 55 60

Ala Trp Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu Asp Leu Ser
65 70 75 80

<210> SEQ ID NO 164
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 164

Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile
1 5 10 15

Asp Lys Lys Val Cys Lys Lys Thr Asp Asn Thr Glu Gly Ser Trp Lys
20 25 30

Cys Thr Gln Thr Gly Asn Asp Gly Gly Asp Lys Glu Phe Ser Lys Thr
35 40 45

Phe Thr Lys Thr Gly Val Asn Glu Ala Thr Lys Gly Lys Ala Trp Pro
50 55 60

Asn Gly His Thr Asp Ser Ala Ala Lys Ala Glu Asp Leu Ser
65 70 75

<210> SEQ ID NO 165
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 165

Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asn Ile
1 5 10 15

Asp Lys Lys Val Cys Lys Lys Thr Gly Asn Asp Ala Asn Ser Trp Lys
20 25 30

Cys Leu Gln Thr Gly Arg Asp Asp Ser Thr Ser Gly Lys Lys Phe Ser
35 40 45

Glu Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala
50 55 60

Trp Pro Asn Gly Asn Glu Ala Ala Lys Ala Glu Asp Leu Ser
65 70 75

<210> SEQ ID NO 166
<211> LENGTH: 80
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 166

Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asn Ile
1 5 10 15

Asp Lys Lys Val Cys Lys Lys Thr Gly Asn Asp Ala Asn Ser Trp Lys
20 25 30

Cys Glu Gln Thr Gly Ser Gly Ala Glu Thr Ser Ala Lys Ala Phe Ser
35 40 45

-continued

Glu Ile Phe Thr Lys Ala Gly Val Asn Glu Ala Thr Lys Gly Lys Ala
50 55 60

Trp Pro Asn Gly His Thr Gly Gly Ala Ala Lys Ala Glu Asp Leu Ser
65 70 75 80

<210> SEQ ID NO 167
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 167

Glu Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile
1 5 10 15

Asp Gly Lys Val Cys Lys Lys Thr Gly Asn Glu Ala Asp Ser Trp Lys
20 25 30

Cys Thr Gln Thr Gly Asn Gly Ser Gly Asn Ala Thr Glu Phe Ser Lys
35 40 45

Ile Phe Thr Lys Lys Asn Val Asp Ala Glu Gly Lys Gly Lys Ala Trp
50 55 60

Pro Asn Gly His Thr Asp Ser Ala Ala Lys Ala Glu Asp Leu Ser
65 70 75

<210> SEQ ID NO 168
<211> LENGTH: 406
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 168

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
1 5 10 15

Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp
20 25 30

Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
35 40 45

Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
50 55 60

Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
65 70 75 80

Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
85 90 95

Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr
100 105 110

Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe
115 120 125

Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp
130 135 140

Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp
145 150 155 160

Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu
165 170 175

Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp
180 185 190

Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala Ala Gly Ser Trp
195 200 205

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Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr Ala Glu Phe Ser
 210 215 220
 Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala
 225 230 235 240
 Trp Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu Asp Leu Ser Ile
 245 250 255
 Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly
 260 265 270
 Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu Ile Arg Ala
 275 280 285
 Val Ser Thr Thr Ser Val Met Leu Asn Gly Cys Tyr Asp Leu Gln Ser
 290 295 300
 Glu Gly Phe Ser Ile Val Pro Tyr Ala Cys Leu Gly Val Gly Ala Asn
 305 310 315 320
 Phe Val Gly Ile Val Asp Gly His Val Thr Pro Lys Leu Ala Tyr Lys
 325 330 335
 Val Lys Ala Gly Leu Ser Tyr Glu Leu Ser Pro Glu Ile Ser Met Phe
 340 345 350
 Ala Gly Gly Phe Tyr His Arg Val Leu Gly Glu Gly Glu Tyr Asp Asp
 355 360 365
 Leu Pro Val Gln Arg Leu Val Asp Asp Ala Thr Thr Asn Lys Thr Lys
 370 375 380
 Glu Phe Ala Lys Ala Ser Phe Lys Met Ala Tyr Thr Gly Ala Glu Ile
 385 390 395 400
 Gly Val Arg Phe Ala Phe
 405

<210> SEQ ID NO 169
 <211> LENGTH: 410
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct
 <400> SEQUENCE: 169

Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
 1 5 10 15
 Ala Leu Ala Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
 20 25 30
 Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
 35 40 45
 Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
 50 55 60
 Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
 65 70 75 80
 Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
 85 90 95
 Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
 100 105 110
 Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
 115 120 125
 Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
 130 135 140
 Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
 145 150 155 160

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Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Thr Ala
 165 170 175
 Leu Gly Lys Met Thr Lys Gly Glu Ala Lys Lys Trp Gly Asn Ala Ile
 180 185 190
 Glu Ser Ala Thr Gly Thr Thr Ser Gly Asp Glu Leu Ser Lys Lys Val
 195 200 205
 Cys Gly Lys Gly Thr Thr Ser Gly Ser Thr Asn Gln Cys Gly Thr Thr
 210 215 220
 Asp Ser Thr Ala Thr Thr Lys Ile Ser Glu Val Phe Thr Glu Gly Thr
 225 230 235 240
 Asp Thr Leu Leu Ser Val Glu Gly Asn Lys Asp Thr Thr Asn Leu Gln
 245 250 255
 Gly Met Ala Asn Asn Ile Asn Asn Leu Ser Lys Glu Asp Lys Ala Val
 260 265 270
 Val Ala Gly Ala Phe Ala Arg Ala Val Glu Gly Ala Glu Val Ile Glu
 275 280 285
 Val Arg Ala Ile Gly Ser Thr Ser Val Met Leu Asn Ala Cys Tyr Asp
 290 295 300
 Leu Leu Thr Asp Gly Ile Gly Val Val Pro Tyr Ala Cys Ala Gly Ile
 305 310 315 320
 Gly Gly Asn Phe Val Ser Val Val Asp Gly His Ile Asn Pro Lys Phe
 325 330 335
 Ala Tyr Arg Val Lys Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu Ile
 340 345 350
 Ser Ala Phe Ala Gly Ala Phe Tyr His Lys Val Leu Gly Asp Gly Asp
 355 360 365
 Tyr Asp Glu Leu Pro Leu Ser His Ile Ser Asp Tyr Thr Gly Thr Ala
 370 375 380
 Gly Lys Asn Lys Asp Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe
 385 390 395 400
 Gly Gly Glu Leu Gly Val Arg Phe Ala Phe
 405 410

<210> SEQ ID NO 170
 <211> LENGTH: 406
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 170

Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
 1 5 10 15
 Ala Leu Val Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
 20 25 30
 Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
 35 40 45
 Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
 50 55 60
 Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
 65 70 75 80
 Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
 85 90 95
 Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
 100 105 110

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Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
115 120 125

Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
130 135 140

Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
145 150 155 160

Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Ala Ala
165 170 175

Leu Gly Lys Met Thr Lys Gly Glu Ala Lys Lys Trp Gly Thr Thr Val
180 185 190

Glu Ala Ala Thr Asn Gly Gln Thr Val Ser Gln Asn Val Cys Lys Gly
195 200 205

Asp Ser Gly Lys Cys Gly Val Asn Ala Asn Ser Gly Ser Thr Thr Ala
210 215 220

Thr Thr Lys Ile Ser Ala Val Phe Thr Glu Gly Thr Asp Thr Ala Thr
225 230 235 240

Gln Leu Ser Ala Asp Thr Asn Asn Val Ser Thr Ser Gly Met Ala Asn
245 250 255

Asn Ile Asn Ser Leu Ser Lys Glu Glu Lys Ala Val Val Ala Gly Ala
260 265 270

Phe Ala Arg Ala Val Glu Gly Ala Glu Val Ile Glu Val Arg Ala Ile
275 280 285

Gly Ser Thr Ser Val Met Leu Asn Ala Cys Tyr Asp Leu Leu Thr Asp
290 295 300

Gly Ile Gly Val Val Pro Tyr Ala Cys Ala Gly Ile Gly Gly Asn Phe
305 310 315 320

Val Ser Val Val Asp Gly His Ile Asn Pro Lys Phe Ala Tyr Arg Val
325 330 335

Lys Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu Ile Ser Ala Ser Ala
340 345 350

Gly Ala Phe Tyr His Lys Val Leu Gly Asp Gly Asp Tyr Asp Glu Leu
355 360 365

Pro Leu Ser His Ile Ser Asp Tyr Thr Gly Thr Ala Gly Lys Asn Lys
370 375 380

Asp Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe Gly Gly Glu Leu
385 390 395 400

Gly Val Arg Phe Ala Phe
405

<210> SEQ ID NO 171

<211> LENGTH: 410

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 171

Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
1 5 10 15

Ala Leu Val Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
20 25 30

Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
35 40 45

Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
50 55 60

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Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
65                               70                               75                               80

Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
                               85                               90                               95

Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
100                               105                               110

Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
115                               120                               125

Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
130                               135                               140

Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
145                               150                               155                               160

Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Thr Ala
165                               170                               175

Leu Gly Lys Met Thr Lys Ser Glu Ala Lys Lys Trp Gly Asn Ala Ile
180                               185                               190

Glu Ser Ala Thr Gly Thr Thr Ser Gly Asp Glu Leu Ser Lys Lys Val
195                               200                               205

Cys Gly Lys Gly Thr Thr Ser Gly Asn Gln Cys Gly Lys Asn Ser Gly
210                               215                               220

Asp Thr Asn Gly Ser Ser Thr Thr Gln His Lys Ile Gly Ala Val Phe
225                               230                               235                               240

Thr Asp Glu Ala Thr Leu Leu Ser Ala Ala Gly Asp Thr Ile Asn Thr
245                               250                               255

Thr Gly Met Ala Gly Asn Ile Asn Ser Leu Thr Lys Asp Glu Lys Ala
260                               265                               270

Ile Val Ala Gly Ala Phe Ala Arg Ala Val Glu Gly Ala Glu Val Ile
275                               280                               285

Glu Val Arg Ala Ile Gly Ser Thr Ser Val Met Leu Asn Ala Cys Tyr
290                               295                               300

Asp Leu Leu Thr Asp Gly Ile Gly Val Val Pro Tyr Ala Cys Ala Gly
305                               310                               315                               320

Ile Gly Gly Asn Phe Val Ser Val Val Asp Gly His Ile Asn Pro Lys
325                               330                               335

Phe Ala Tyr Arg Val Lys Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu
340                               345                               350

Ile Ser Ala Phe Ala Gly Ala Phe Tyr His Lys Val Leu Gly Asp Gly
355                               360                               365

Asp Tyr Asp Glu Leu Pro Leu Ser His Ile Ser Asp Tyr Thr Thr Ala
370                               375                               380

Gly Lys Asn Lys Asp Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe
385                               390                               395                               400

Gly Gly Glu Leu Gly Val Arg Phe Ala Phe
405                               410

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<210> SEQ ID NO 172
<211> LENGTH: 410
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 172

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Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
1           5           10           15

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Ala Leu Val Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
 20 25 30
 Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
 35 40 45
 Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
 50 55 60
 Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
 65 70 75 80
 Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
 85 90 95
 Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
 100 105 110
 Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
 115 120 125
 Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
 130 135 140
 Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
 145 150 155 160
 Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Thr Ala
 165 170 175
 Leu Gly Lys Met Thr Lys Ser Glu Ala Lys Lys Trp Gly Asn Ala Ile
 180 185 190
 Glu Ser Ala Thr Gly Thr Thr Ser Gly Asp Glu Leu Ser Lys Lys Val
 195 200 205
 Cys Gly Lys Gly Glu Gly Ser Asn Gly Thr Lys Lys Cys Gly Thr Thr
 210 215 220
 Asp Ser Thr Ala Thr Thr Lys Ile Ser Glu Val Phe Thr Glu Gly Thr
 225 230 235 240
 Asp Thr Leu Leu Ser Val Glu Gly Asn Lys Asp Thr Ile Asn Leu Gln
 245 250 255
 Gly Met Ala Asn Asn Ile Asn Asn Leu Ser Lys Glu Asp Lys Ala Val
 260 265 270
 Val Ala Gly Ala Phe Ala Arg Ala Val Glu Gly Ala Glu Val Ile Glu
 275 280 285
 Val Arg Ala Ile Gly Ser Thr Ser Val Met Leu Asn Ala Cys Tyr Asp
 290 295 300
 Leu Leu Thr Asp Gly Ile Gly Val Val Pro Tyr Ala Cys Ala Gly Ile
 305 310 315 320
 Gly Gly Asn Phe Val Ser Val Val Asp Gly His Ile Asn Pro Lys Phe
 325 330 335
 Ala Tyr Arg Val Lys Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu Ile
 340 345 350
 Ser Ala Phe Ala Gly Ala Phe Tyr His Lys Val Leu Gly Asp Ser Gly
 355 360 365
 Tyr Asp Glu Leu Pro Leu Ser His Ile Ser Asp Tyr Thr Gly Thr Ala
 370 375 380
 Gly Lys Asn Lys Asp Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe
 385 390 395 400
 Gly Gly Glu Leu Gly Val Arg Phe Ala Phe
 405 410

<210> SEQ ID NO 173

<211> LENGTH: 409

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 173

Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
 1             5             10             15

Ala Leu Val Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
 20             25             30

Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
 35             40             45

Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
 50             55             60

Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
 65             70             75             80

Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
 85             90             95

Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
 100            105            110

Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
 115            120            125

Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
 130            135            140

Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
 145            150            155            160

Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Thr Ala
 165            170            175

Leu Gly Lys Met Thr Lys Ser Glu Ala Lys Lys Trp Gly Asn Ala Ile
 180            185            190

Glu Ser Ala Thr Gly Thr Thr Ser Gly Asp Glu Leu Ser Lys Lys Val
 195            200            205

Cys Gly Lys Gly Thr Gly Ser Ser Gly Ser Ser Gly Asn Lys Cys Gly
 210            215            220

Thr Thr Asp Ser Thr Ala Thr Thr Lys Ile Ser Ala Val Phe Thr Asp
 225            230            235            240

Glu Ala Thr Leu Leu Ser Ala Ala Gly Asp Thr Ile Asn Thr Thr Gly
 245            250            255

Met Ala Gly Asn Ile Asn Ser Leu Ser Lys Glu Asp Lys Ala Val Val
 260            265            270

Ala Gly Ala Phe Ala Arg Ala Val Glu Gly Ala Glu Val Ile Glu Val
 275            280            285

Arg Ala Ile Gly Ser Thr Ser Val Met Leu Asn Ala Cys Tyr Asp Leu
 290            295            300

Leu Thr Asp Gly Ile Gly Val Val Pro Tyr Ala Cys Ala Gly Ile Gly
 305            310            315            320

Gly Asn Phe Val Ser Val Val Asp Gly His Ile Asn Pro Lys Phe Ala
 325            330            335

Tyr Arg Val Lys Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu Ile Ser
 340            345            350

Ala Phe Ala Gly Ala Phe Tyr His Lys Val Leu Gly Asp Gly Asp Tyr
 355            360            365

Asp Glu Leu Pro Leu Ser His Ile Ser Asp Tyr Thr Gly Thr Ala Gly
 370            375            380

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Lys Asn Lys Asp Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe Gly
385 390 395 400

Gly Glu Leu Gly Val Arg Phe Ala Phe
405

<210> SEQ ID NO 174

<211> LENGTH: 405

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 174

Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
1 5 10 15

Ala Leu Val Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
20 25 30

Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
35 40 45

Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
50 55 60

Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
65 70 75 80

Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
85 90 95

Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
100 105 110

Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
115 120 125

Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
130 135 140

Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
145 150 155 160

Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Thr Ala
165 170 175

Leu Gly Lys Met Thr Lys Gly Glu Ala Lys Lys Trp Gly Asn Ala Val
180 185 190

Glu Asn Ala Thr Asn Gly Asp Lys Val Ser Gln Asn Val Cys Lys Gly
195 200 205

Thr Gly Ser Thr Gly Ser Ser Gly Asn Lys Cys Gly Thr Thr Asp Ser
210 215 220

Thr Ala Thr Thr Lys Ile Ser Ala Val Phe Thr Asp Glu Ala Thr Leu
225 230 235 240

Leu Ser Ala Ala Gly Asp Thr Ile Asn Thr Thr Gly Met Ala Gly Asn
245 250 255

Ile Asn Ser Leu Thr Lys Asp Glu Lys Ala Ile Val Ala Gly Ala Phe
260 265 270

Ala Arg Ala Val Glu Gly Ala Glu Val Ile Glu Val Arg Ala Ile Gly
275 280 285

Ser Thr Ser Val Met Leu Asn Ala Cys Tyr Asp Leu Leu Thr Asp Gly
290 295 300

Ile Gly Val Val Pro Tyr Ala Cys Ala Gly Ile Gly Gly Asn Phe Val
305 310 315 320

Ser Val Val Asp Gly His Ile Asn Pro Lys Phe Ala Tyr Arg Val Lys
325 330 335

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Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu Ile Ser Ala Phe Ala Gly
 340 345 350

Ala Phe Tyr His Lys Val Leu Gly Asp Gly Asp Tyr Asp Glu Leu Pro
 355 360 365

Leu Ser His Ile Ser Asp Tyr Thr Gly Thr Ala Gly Lys Asn Lys Asp
 370 375 380

Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe Gly Gly Glu Leu Gly
 385 390 395 400

Val Arg Phe Ala Phe
 405

<210> SEQ ID NO 175
 <211> LENGTH: 407
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 175

Met Ser Ala Val Ser Asn Arg Lys Leu Pro Leu Gly Gly Val Leu Met
 1 5 10 15

Ala Leu Val Ala Ala Val Ala Pro Ile His Ser Leu Leu Ala Ala Pro
 20 25 30

Ala Ala Gly Ala Gly Ala Gly Gly Glu Gly Leu Phe Ser Gly Ala Gly
 35 40 45

Ala Gly Ser Phe Tyr Ile Gly Leu Asp Tyr Ser Pro Ala Phe Gly Ser
 50 55 60

Ile Lys Asp Phe Lys Val Gln Glu Ala Gly Gly Thr Thr Arg Gly Val
 65 70 75 80

Phe Pro Tyr Lys Arg Asp Ala Ala Gly Arg Val Asp Phe Lys Val His
 85 90 95

Asn Phe Asp Trp Ser Ala Pro Glu Pro Lys Ile Ser Phe Lys Asp Ser
 100 105 110

Met Leu Thr Ala Leu Glu Gly Ser Ile Gly Tyr Ser Ile Gly Gly Ala
 115 120 125

Arg Val Glu Val Glu Val Gly Tyr Glu Arg Phe Val Ile Lys Gly Gly
 130 135 140

Lys Lys Ser Asn Glu Asp Thr Ala Ser Val Phe Leu Leu Gly Lys Glu
 145 150 155 160

Leu Ala Tyr Asp Thr Ala Arg Gly Gln Val Asp Arg Leu Ala Thr Ala
 165 170 175

Leu Gly Lys Met Thr Lys Ser Glu Ala Lys Lys Trp Gly Asn Ala Val
 180 185 190

Glu Asn Ala Thr Asn Gly Asp Lys Val Ser Gln Asn Val Cys Lys Gly
 195 200 205

Thr Gly Ser Thr Gly Ser Ser Gly Asn Lys Cys Gly Thr Thr Asp Ser
 210 215 220

Thr Ala Thr Thr Lys Ile Ser Ala Val Phe Thr Glu Asp Ala Ala Ala
 225 230 235 240

Gln Leu Ser Thr Met Asp Asn Thr Thr Ile Asp Thr Thr Gly Met Ala
 245 250 255

Asn Asn Ile Asn Ser Leu Thr Lys Asp Glu Lys Ala Ile Val Ala Gly
 260 265 270

Ala Phe Ala Arg Ala Val Glu Gly Ala Glu Val Ile Glu Val Arg Ala
 275 280 285

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Ile Gly Ser Thr Ser Val Met Leu Asn Ala Cys Tyr Asp Leu Leu Thr
 290                295                300

Asp Gly Ile Gly Val Val Pro Tyr Ala Cys Ala Gly Ile Gly Gly Asn
 305                310                315                320

Phe Val Ser Val Val Asp Gly His Ile Asn Pro Lys Phe Ala Tyr Arg
                325                330                335

Val Lys Ala Gly Leu Ser Tyr Ala Leu Thr Pro Glu Ile Ser Ala Phe
                340                345                350

Ala Gly Ala Phe Tyr His Lys Val Leu Gly Asp Gly Asp Tyr Asp Glu
 355                360                365

Leu Pro Leu Ser His Ile Ser Asp Tyr Thr Gly Thr Ala Gly Lys Asn
 370                375                380

Lys Asp Thr Gly Ile Ala Ser Phe Asn Phe Ala Tyr Phe Gly Gly Glu
 385                390                395                400

Leu Gly Val Arg Phe Ala Phe
 405

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<210> SEQ ID NO 176
<211> LENGTH: 431
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 176

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Met Arg Lys Gly Lys Ile Ile Leu Gly Ser Val Met Met Ser Met Ala
 1                5                10                15

Ile Val Met Ala Gly Asn Asp Val Arg Ala His Asp Asp Val Ser Ala
                20                25                30

Leu Glu Thr Gly Gly Ala Gly Tyr Phe Tyr Val Gly Leu Asp Tyr Ser
 35                40                45

Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile Arg Glu Ser Asn Gly
 50                55                60

Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp Gly Lys Ser Val Lys
 65                70                75                80

Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile Gly
                85                90                95

Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly Ser Val Gly Tyr Gly
                100                105                110

Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Arg Phe Lys
 115                120                125

Thr Lys Gly Ile Arg Asp Ser Gly Ser Lys Glu Asp Glu Ala Asp Thr
 130                135                140

Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp Val Val Thr Gly Gln
 145                150                155                160

Thr Asp Asn Leu Ala Ala Ala Leu Ala Lys Thr Ser Gly Lys Asp Ile
                165                170                175

Val Gln Phe Ala Lys Ala Val Glu Ile Ser Asn Ser Gly Ile Gly Lys
                180                185                190

Lys Val Cys Glu Thr Lys Arg Lys Asp Gly Asp Thr Thr Asn Arg Phe
 195                200                205

Ala Lys Tyr Ile Val Gly Ala Gly Asp Ser Ser Asn Ala Gly Thr Ser
 210                215                220

Leu Cys Gly Gly Lys Asn Gln Lys Ser Ser Asp Thr Asp Thr Gly Val
 225                230                235                240

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Glu	Lys	Ala	Gln	Ala	Leu	His	Asp	Phe	Val	Ser	Asn	Thr	Leu	Ser	Asp
				245					250					255	
Gly	Thr	Lys	Asn	Trp	Pro	Thr	Ser	Ser	Glu	Thr	Ser	Lys	Ser	Asn	Asn
			260					265					270		
Asp	Asn	Ala	Lys	Ala	Val	Ala	Gly	Asp	Leu	Thr	Lys	Lys	Leu	Thr	Pro
		275					280					285			
Glu	Glu	Lys	Thr	Ile	Val	Ala	Gly	Leu	Leu	Ala	Lys	Thr	Ile	Glu	Gly
	290					295					300				
Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val	Ser	Ser	Thr	Ser	Val	Met	Val
305					310					315					320
Asn	Ala	Cys	Tyr	Asp	Leu	Leu	Ser	Glu	Gly	Leu	Gly	Val	Val	Pro	Tyr
				325					330					335	
Ala	Cys	Val	Gly	Leu	Gly	Gly	Asn	Phe	Val	Gly	Val	Val	Asp	Gly	His
			340					345					350		
Ile	Thr	Pro	Lys	Leu	Ala	Tyr	Arg	Leu	Lys	Ala	Gly	Leu	Ser	Tyr	Gln
		355					360					365			
Leu	Ser	Pro	Glu	Ile	Ser	Ala	Phe	Ala	Gly	Gly	Phe	Tyr	His	Arg	Val
	370					375					380				
Val	Gly	Asp	Gly	Val	Tyr	Asp	Asp	Leu	Pro	Ala	Gln	Arg	Leu	Val	Asp
385					390				395						400
Asp	Thr	Ser	Pro	Ala	Gly	Arg	Thr	Lys	Asp	Thr	Ala	Ile	Ala	Asn	Phe
				405					410					415	
Ser	Met	Ala	Tyr	Val	Gly	Gly	Glu	Phe	Gly	Val	Arg	Phe	Ala	Phe	
			420					425					430		

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<210> SEQ ID NO 177
<211> LENGTH: 433
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
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<400> SEQUENCE: 177

Met 1	Met	Ser	Met	Ala 5	Ile	Val	Met	Ala	Gly 10	Ser	Asp	Val	Arg	Ala 15	His
Asp	Asp	Val	Ser 20	Ala	Leu	Asp	Thr	Gly 25	Gly	Ala	Gly	Tyr	Phe	Tyr	Val
Gly	Leu	Asp 35	Tyr	Ser	Pro	Ala	Phe 40	Ser	Lys	Ile	Arg	Asp 45	Phe	Ser	Ile
Arg	Glu 50	Ser	Asn	Gly	Glu	Thr 55	Lys	Ala	Val	Tyr	Pro 60	Tyr	Leu	Lys	Asp
Gly 65	Lys	Ser	Val	Lys	Leu 70	Glu	Ser	His	Lys	Phe 75	Asp	Trp	Asn	Thr	Pro 80
Asp	Pro	Arg	Ile 85	Gly	Phe	Lys	Asp	Asn	Met 90	Leu	Val	Ala	Met	Glu	Gly
Ser	Val	Gly	Tyr 100	Gly	Ile	Gly	Gly	Ala 105	Arg	Val	Glu	Leu	Glu	Ile	Gly
Tyr	Glu	Arg	Phe 115	Lys	Thr	Lys	Gly 120	Ile	Arg	Asp	Ser	Gly 125	Ser	Lys	Glu
Asp	Glu 130	Ala	Asp	Thr	Val	Tyr 135	Leu	Leu	Ala	Lys	Glu 140	Leu	Ala	Tyr	Asp
Val 145	Val	Thr	Gly	Gln	Thr 150	Asp	Lys	Leu	Thr	Ala 155	Ala	Leu	Ala	Lys	Thr 160
Ser	Gly	Lys	Asp 165	Ile	Val	Gln	Phe	Ala	Lys 170	Thr	Leu	Gly	Ile	Ser	His

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Ser Glu Ile Asp Lys Lys Val Cys Ser Gly Ser His Ala Lys Gly Asn
   180                               185                               190

Ser Glu Thr Thr Lys Asn Asn Thr Val Ala Ser Tyr Thr Glu Lys Pro
   195                               200                               205

Thr Ala Ala Thr Ala Thr Ala Gln Cys Ser Gly Phe Pro Asp Glu Ala
   210                               215                               220

Ala Gly Asn Lys Ala Gly Gly Leu Asn Arg Phe Val Ser Glu Thr Lys
   225                               230                               235                               240

Val Glu Glu Gly Lys Asn Trp Pro Thr Gly Lys Ile His Ser Gly Ser
   245                               250                               255

Ser Thr Asn Asn Val Asp Gly Thr His Asn Gly Asn Ala Lys Ala Val
   260                               265                               270

Ala Thr Asp Leu Val Asn Leu Asn Arg Asp Glu Lys Thr Ile Val Ala
   275                               280                               285

Gly Leu Leu Ala Lys Thr Ile Glu Gly Gly Glu Val Val Glu Ile Arg
   290                               295                               300

Ala Val Ser Ser Thr Ser Val Met Val Asn Ala Cys Tyr Asp Leu Leu
   305                               310                               315                               320

Ser Glu Gly Leu Gly Val Val Pro Tyr Ala Cys Val Gly Leu Gly Gly
   325                               330                               335

Asn Phe Val Gly Val Val Asp Gly His Ile Thr Pro Lys Leu Ala Tyr
   340                               345                               350

Arg Leu Lys Ala Gly Leu Ser Tyr Gln Leu Ser Pro Glu Ile Ser Ala
   355                               360                               365

Phe Ala Gly Gly Phe Tyr His Arg Val Val Gly Asp Gly Val Tyr Asp
   370                               375                               380

Asp Leu Pro Ala Gln Arg Leu Val Asp Asp Thr Ser Pro Ala Gly Arg
   385                               390                               395                               400

Thr Lys Asp Thr Ala Ile Ala Asn Phe Ser Met Ala Tyr Val Gly Ala
   405                               410                               415

Ser Phe Gln Pro Tyr Tyr Ala Val Leu Leu Val Glu Leu Tyr Glu Tyr
   420                               425                               430

```

Arg

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<210> SEQ ID NO 178
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 178

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Met Met Ser Met Ala Ile Val Met Ala Gly Asn Asp Val Arg Ala His
 1          5          10          15

Asp Asp Val Ser Ala Leu Glu Thr Gly Gly Ala Gly Tyr Phe Tyr Val
 20          25          30

Gly Leu Asp Tyr Ser Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile
 35          40          45

Arg Glu Ser Asn Gly Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp
 50          55          60

Gly Lys Ser Val Lys Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro
 65          70          75          80

Asp Pro Arg Ile Gly Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly
 85          90          95

Ser Val Gly Tyr Gly Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly

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100					105					110					
Tyr	Glu	Arg	Phe	Lys	Thr	Lys	Gly	Ile	Arg	Asp	Ser	Gly	Ser	Lys	Glu
	115						120					125			
Asp	Glu	Ala	Asp	Thr	Val	Tyr	Leu	Leu	Ala	Lys	Glu	Leu	Ala	Tyr	Asp
	130					135					140				
Val	Val	Thr	Gly	Gln	Thr	Asp	Lys	Leu	Thr	Ala	Ala	Leu	Ala	Lys	Thr
	145					150					155				160
Ser	Gly	Lys	Asp	Ile	Val	Gln	Phe	Ala	Asn	Ala	Val	Lys	Ile	Ser	Ser
			165						170					175	
Ser	Ala	Ile	Asp	Gly	Lys	Val	Cys	Thr	Gly	Ser	His	Ala	Asp	Leu	Ala
			180						185					190	
Pro	Gly	Thr	Asn	Ala	Gly	Lys	Lys	Phe	Val	Val	Asn	Pro	Glu	Ala	Ser
			195				200					205			
Gly	Ser	Thr	Asp	Gly	Asp	Thr	Ser	Gln	Cys	Ser	Gly	Leu	Gly	His	Ser
	210					215					220				
Ser	Gly	Val	Thr	Gln	Asn	Pro	Lys	Leu	Phe	Ser	Thr	Phe	Val	Asp	Thr
	225					230					235				240
Val	Lys	Ile	Ala	Glu	Asp	Lys	Asn	Trp	Pro	Thr	Gly	Arg	Ala	Lys	Ser
			245						250					255	
Asn	Thr	Ser	Leu	Lys	Thr	Gly	Asp	Thr	Asn	Ser	Asn	Ala	Lys	Ala	Val
			260					265						270	
Ala	Thr	Asp	Leu	Val	Gln	Glu	Leu	Thr	Pro	Glu	Glu	Lys	Thr	Ile	Val
			275				280						285		
Ala	Gly	Leu	Leu	Ala	Lys	Thr	Ile	Glu	Gly	Gly	Glu	Val	Val	Glu	Ile
	290					295					300				
Arg	Ala	Val	Ser	Ser	Thr	Phe	Ile	Arg	Ile	Arg	Asp	Lys	Leu	Ile	Ser
	305					310					315				320
Leu	Leu	Pro	Leu	Leu	Thr	Trp	Glu	Trp	Lys	Ile	Val	His	Ser	Val	Cys
			325					330						335	
Ala	Ala	Gly	Val	Arg	Tyr	Ser	Asn	Leu	Arg	Leu	Leu	Val	Leu	Leu	Ser
			340					345						350	
Gly	Thr	Trp	Phe	Ile	Pro	Gly									
			355												

<210> SEQ ID NO 179

<211> LENGTH: 422

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 179

Met	Met	Ser	Leu	Ala	Ile	Val	Met	Ala	Gly	Asn	Asp	Val	Arg	Ala	His
1				5					10					15	
Asp	Asp	Val	Ser	Ala	Leu	Asp	Thr	Gly	Gly	Ala	Gly	Tyr	Phe	Tyr	Val
		20						25					30		
Gly	Leu	Asp	Tyr	Ser	Pro	Ala	Phe	Ser	Lys	Ile	Arg	Asp	Phe	Ser	Ile
		35					40					45			
Arg	Glu	Ser	Asn	Gly	Glu	Thr	Lys	Ala	Val	Tyr	Pro	Tyr	Leu	Lys	Asp
	50					55					60				
Gly	Lys	Ser	Val	Lys	Leu	Glu	Ser	His	Lys	Phe	Asp	Trp	Asn	Thr	Pro
	65			70							75			80	
Asp	Pro	Arg	Ile	Gly	Phe	Lys	Asp	Asn	Met	Leu	Val	Ala	Met	Glu	Gly
			85					90						95	
Ser	Val	Gly	Tyr	Gly	Ile	Gly	Gly	Ala	Arg	Val	Glu	Leu	Glu	Ile	Gly

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100					105					110					
Tyr	Glu	Arg	Phe	Lys	Thr	Lys	Gly	Ile	Arg	Asp	Ser	Gly	Ser	Lys	Glu
	115						120					125			
Asp	Glu	Ala	Asp	Thr	Val	Tyr	Leu	Leu	Ala	Lys	Glu	Leu	Ala	Tyr	Asp
	130					135					140				
Val	Val	Thr	Gly	Gln	Thr	Asp	Lys	Leu	Thr	Ala	Ala	Leu	Ala	Lys	Thr
	145					150					155				160
Ser	Gly	Lys	Asp	Ile	Val	Gln	Phe	Ala	Asn	Ala	Val	Lys	Ile	Thr	Asn
			165						170					175	
Ser	Thr	Ile	Asp	Gly	Lys	Val	Cys	Ser	Gly	Lys	His	Ala	Ala	Leu	Val
			180						185					190	
Pro	Asn	Lys	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Ala	Lys	Glu	Ser	Asn	Thr
		195					200					205			
Asn	Ala	His	Lys	Thr	Ala	Gln	Cys	Ser	Gly	Leu	Ala	Asp	Ser	Ala	Ala
	210					215					220				
Thr	Gly	Pro	Lys	Ser	Phe	Ser	Gly	Phe	Val	Gly	Ala	Val	Lys	Val	Gly
	225					230					235				240
Glu	Gly	Lys	Asn	Trp	Pro	Thr	Gly	Arg	Ala	Ala	Ser	Ala	Thr	Ser	Asn
			245						250					255	
Glu	Thr	Val	Val	Gly	Pro	Thr	Asn	Ser	Asn	Ala	Thr	Ala	Val	Ala	Lys
			260						265				270		
Asp	Leu	Val	Ala	Leu	Asn	Ser	Asp	Glu	Lys	Thr	Ile	Val	Ala	Gly	Leu
		275					280					285			
Leu	Ala	Lys	Thr	Ile	Glu	Gly	Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val
	290					295					300				
Ser	Ser	Thr	Ser	Val	Met	Val	Asn	Ala	Cys	Tyr	Asp	Leu	Leu	Ser	Glu
	305					310					315				320
Gly	Leu	Gly	Val	Val	Pro	Tyr	Ala	Cys	Val	Gly	Leu	Gly	Gly	Asn	Phe
			325						330					335	
Val	Gly	Val	Val	Asp	Gly	His	Ile	Thr	Pro	Lys	Leu	Ala	Tyr	Arg	Leu
			340					345					350		
Lys	Ala	Gly	Leu	Ser	Tyr	Gln	Leu	Ser	Pro	Glu	Ile	Ser	Ala	Phe	Ala
		355					360					365			
Gly	Gly	Phe	Tyr	His	Arg	Val	Val	Gly	Asp	Gly	Val	Tyr	Asp	Asp	Leu
	370					375					380				
Pro	Ala	Gln	Arg	Leu	Val	Asp	Asp	Thr	Ser	Pro	Ala	Gly	Arg	Thr	Lys
	385					390					395				400
Asp	Thr	Ala	Ile	Ala	Asn	Phe	Ser	Met	Ala	Tyr	Val	Gly	Gly	Glu	Phe
			405						410					415	
Gly	Val	Arg	Phe	Ala	Phe										
			420												

<210> SEQ ID NO 180

<211> LENGTH: 355

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 180

Met	Met	Ser	Met	Ala	Ile	Val	Met	Ala	Gly	Asn	Asp	Val	Arg	Ala	His
1				5					10					15	

Asp	Asp	Val	Ser	Ala	Leu	Glu	Thr	Gly	Gly	Ala	Gly	Tyr	Phe	Tyr	Val
		20						25					30		

Gly	Leu	Asp	Tyr	Ser	Pro	Ala	Phe	Ser	Lys	Ile	Arg	Asp	Phe	Ser	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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35					40					45					
Arg	Glu	Ser	Asn	Gly	Glu	Thr	Lys	Ala	Val	Tyr	Pro	Tyr	Leu	Lys	Asp
50					55					60					
Gly	Lys	Ser	Val	Lys	Leu	Glu	Ser	His	Lys	Phe	Asp	Trp	Asn	Thr	Pro
65				70					75					80	
Asp	Pro	Arg	Ile	Gly	Phe	Lys	Asp	Asn	Met	Leu	Val	Ala	Met	Glu	Gly
				85					90					95	
Ser	Val	Gly	Tyr	Gly	Ile	Gly	Gly	Ala	Arg	Val	Glu	Leu	Glu	Ile	Gly
			100					105					110		
Tyr	Glu	Arg	Phe	Lys	Thr	Lys	Gly	Ile	Arg	Asp	Ser	Gly	Ser	Lys	Glu
			115				120					125			
Asp	Glu	Ala	Asp	Thr	Val	Tyr	Leu	Leu	Ala	Lys	Glu	Leu	Ala	Tyr	Asp
	130					135					140				
Val	Val	Thr	Gly	Gln	Thr	Asp	Asn	Leu	Ala	Ala	Ala	Leu	Ala	Lys	Thr
	145			150					155					160	
Ser	Gly	Lys	Asp	Ile	Val	Gln	Phe	Ala	Lys	Ala	Val	Glu	Ile	Ser	Asn
			165					170						175	
Ser	Thr	Ile	Gly	Asp	Lys	Val	Cys	Arg	Thr	Arg	Tyr	Asp	Thr	Ala	Lys
			180					185					190		
Lys	Asp	His	Tyr	Ala	Lys	Tyr	Ala	Lys	Thr	Thr	Asp	Lys	Gly	Ser	Ala
			195				200					205			
Ser	Lys	Asn	Asp	Thr	Ser	Leu	Cys	Gly	Asp	Ile	Gly	His	Ser	Thr	Val
	210					215					220				
Thr	Ser	Gly	His	Ser	Thr	Thr	Pro	Gln	Val	Leu	Lys	Asn	Phe	Ile	Ser
	225			230					235					240	
Ala	Thr	Leu	Gly	Asn	Gly	Ser	Gln	Asn	Trp	Pro	Thr	Ser	Thr	Gly	Thr
			245					250						255	
Gly	Ser	Ser	Thr	Asn	Asp	Asn	Ala	Glu	Ala	Val	Ala	Lys	Asp	Leu	Thr
			260				265						270		
Lys	Leu	Thr	Thr	Glu	Glu	Lys	Thr	Ile	Val	Ala	Gly	Leu	Leu	Ala	Lys
	275						280					285			
Thr	Ile	Glu	Gly	Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val	Ser	Ser	Thr
	290					295					300				
Ser	Val	Met	Val	Asn	Ala	Cys	Tyr	Asp	Leu	Leu	Ser	Glu	Gly	Leu	Gly
	305			310					315					320	
Val	Val	Pro	Tyr	Ala	Cys	Val	Gly	Leu	Gly	Gly	Asn	Phe	Val	Gly	Val
			325					330						335	
Val	Asp	Gly	Thr	Arg	Cys	Thr	Ile	Arg	Pro	Ser	Leu	Thr	Leu	Tyr	Ala
			340				345						350		
His	Ser	Lys													
		355													

<210> SEQ ID NO 181

<211> LENGTH: 435

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 181

Met	Arg	Lys	Gly	Lys	Ile	Ile	Leu	Gly	Ser	Val	Met	Met	Ser	Met	Ala
1				5					10					15	

Ile	Val	Met	Ala	Gly	Asn	Asp	Val	Arg	Ala	His	Asp	Asp	Val	Ser	Ala
		20					25						30		

Leu	Glu	Thr	Gly	Gly	Ala	Gly	Tyr	Phe	Tyr	Val	Gly	Leu	Asp	Tyr	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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35					40					45					
Pro	Ala	Phe	Ser	Lys	Ile	Arg	Asp	Phe	Ser	Ile	Arg	Glu	Ser	Asn	Gly
50						55					60				
Glu	Thr	Lys	Ala	Val	Tyr	Pro	Tyr	Leu	Lys	Asp	Gly	Lys	Ser	Val	Lys
65					70					75					80
Leu	Glu	Ser	Asn	Lys	Phe	Asp	Trp	Asn	Thr	Pro	Asp	Pro	Arg	Ile	Gly
				85					90					95	
Phe	Lys	Asp	Asn	Met	Leu	Val	Ala	Met	Glu	Gly	Ser	Val	Gly	Tyr	Gly
			100					105					110		
Ile	Gly	Gly	Ala	Arg	Val	Glu	Leu	Glu	Ile	Gly	Tyr	Glu	Arg	Phe	Lys
		115					120					125			
Thr	Lys	Gly	Ile	Arg	Asp	Ser	Gly	Ser	Lys	Glu	Asp	Glu	Ala	Asp	Thr
	130					135					140				
Val	Tyr	Leu	Leu	Ala	Lys	Glu	Leu	Ala	Tyr	Asp	Val	Val	Thr	Gly	Gln
145					150					155					160
Thr	Asp	Lys	Leu	Thr	Ala	Ala	Leu	Ala	Lys	Thr	Ser	Gly	Lys	Asp	Ile
			165						170					175	
Val	Gln	Phe	Ala	Lys	Ala	Val	Gly	Val	Ser	His	Pro	Gly	Ile	Asp	Lys
		180						185					190		
Lys	Val	Cys	Asp	Gly	Gly	His	Ala	Arg	Gly	Lys	Lys	Ser	Gly	Asp	Asn
	195						200					205			
Gly	Ser	Leu	Ala	Asp	Tyr	Thr	Asp	Gly	Gly	Ala	Ser	Gln	Thr	Asn	Lys
	210					215					220				
Thr	Ala	Gln	Cys	Ser	Gly	Met	Gly	Thr	Gly	Lys	Ala	Gly	Lys	Arg	Gly
225					230					235					240
Leu	Gly	Leu	Thr	Glu	Phe	Val	Asn	Lys	Thr	Lys	Val	Gly	Glu	Gly	Lys
			245						250					255	
Asn	Trp	Pro	Thr	Gly	Tyr	Val	Asn	Asp	Gly	Asp	Asn	Val	Asn	Val	Leu
		260						265					270		
Gly	Asp	Thr	Asn	Gly	Asn	Ala	Glu	Ala	Val	Ala	Lys	Asp	Leu	Val	Gln
	275						280					285			
Glu	Leu	Thr	Pro	Glu	Glu	Lys	Thr	Ile	Val	Ala	Gly	Leu	Leu	Ala	Lys
	290					295					300				
Thr	Ile	Glu	Gly	Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val	Ser	Ser	Thr
305					310					315					320
Ser	Val	Met	Val	Asn	Ala	Cys	Tyr	Asp	Leu	Leu	Ser	Glu	Gly	Leu	Gly
			325						330					335	
Val	Val	Pro	Tyr	Ala	Cys	Val	Gly	Leu	Gly	Gly	Asn	Phe	Val	Gly	Val
		340						345					350		
Val	Asp	Gly	His	Ile	Thr	Pro	Lys	Leu	Ala	Tyr	Arg	Leu	Lys	Ala	Gly
	355						360					365			
Leu	Ser	Tyr	Gln	Leu	Ser	Pro	Glu	Ile	Ser	Ala	Phe	Ala	Gly	Gly	Phe
	370					375					380				
Tyr	His	Arg	Val	Val	Gly	Asp	Gly	Val	Tyr	Asp	Asp	Leu	Pro	Ala	Gln
385					390					395					400
Arg	Leu	Val	Asp	Asp	Thr	Ser	Pro	Ala	Gly	Arg	Thr	Lys	Asp	Thr	Ala
			405						410					415	
Ile	Ala	Asn	Phe	Ser	Met	Ala	Tyr	Val	Gly	Gly	Glu	Phe	Gly	Val	Arg
		420						425					430		
Phe	Ala	Phe													
	435														

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<211> LENGTH: 432
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 182

Met Arg Lys Gly Lys Ile Ile Leu Gly Ser Val Met Met Ser Met Ala
1      5      10      15

Ile Val Met Ala Gly Asn Asp Val Arg Ala His Asp Asp Val Ser Ala
20     25     30

Leu Glu Thr Gly Gly Ala Gly Tyr Phe Tyr Ile Gly Leu Asp Tyr Ser
35     40     45

Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile Arg Glu Ser Asn Gly
50     55     60

Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp Gly Lys Ser Val Lys
65     70     75     80

Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile Gly
85     90     95

Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly Ser Val Gly Tyr Gly
100    105    110

Ile Gly Gly Ala Arg Val Glu Leu Gly Ile Gly Tyr Glu Arg Phe Lys
115    120    125

Thr Lys Gly Ile Arg Asp Ser Gly Ser Lys Glu Asp Glu Ala Asp Thr
130    135    140

Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp Val Val Thr Gly Gln
145    150    155    160

Thr Asp Asn Leu Ala Ala Ala Leu Ala Lys Thr Ser Gly Lys Asp Ile
165    170    175

Val Gln Phe Ala Asn Ala Val Lys Ile Ser Ser Pro Glu Ile Asp Gly
180    185    190

Lys Val Cys Ser Gly Asp His Ala Ala Ile Thr Lys Ala Lys Gly Lys
195    200    205

Lys Tyr Val Ala Glu Leu Ser Thr Thr His Ser Asp Glu Glu Thr Thr
210    215    220

Gln Cys Ser Gly Leu Gly Asn Thr Thr Gly Ala Thr Gly Pro Lys Thr
225    230    235    240

Leu Ser Gly Phe Val Asn Thr Val Lys Val Gly Glu Gly Lys Asn Trp
245    250    255

Pro Arg Gly Arg Gly Ser Asn Gly Ser Ser Gln Asn Val Glu Gly Glu
260    265    270

Pro Asn Ser Asn Ala Asn Ala Met Ala Lys Asp Leu Leu Gly Leu Asn
275    280    285

Arg Asp Glu Lys Thr Ile Val Thr Gly Leu Leu Ala Lys Thr Ile Glu
290    295    300

Gly Gly Glu Val Val Glu Ile Arg Ala Val Ser Ser Thr Ser Val Met
305    310    315    320

Val Asn Ala Cys Tyr Asp Leu Leu Ser Glu Gly Leu Gly Val Val Pro
325    330    335

Tyr Ala Cys Val Gly Leu Gly Gly Asn Phe Val Gly Val Val Asp Gly
340    345    350

His Ile Thr Pro Lys Leu Ala Tyr Arg Leu Lys Ala Gly Leu Ser Tyr
355    360    365

Gln Leu Ser Pro Glu Ile Ser Ala Phe Ala Gly Gly Phe Tyr His Arg
370    375    380

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Val Val Gly Asp Gly Val Tyr Asp Asp Leu Pro Ala Gln Arg Leu Val
385 390 395 400

Asp Asp Thr Ser Pro Ala Gly Arg Thr Lys Asp Thr Ala Ile Ala Asn
405 410 415

Phe Ser Met Ala Tyr Val Gly Gly Glu Phe Gly Val Arg Phe Ala Phe
420 425 430

<210> SEQ ID NO 183

<211> LENGTH: 427

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 183

Met Arg Lys Gly Lys Ile Ile Leu Gly Ser Val Met Met Ser Met Ala
1 5 10 15

Ile Val Met Ala Gly Ser Asp Val Arg Ala His Asp Asp Val Ser Ala
20 25 30

Leu Asp Thr Gly Gly Ala Gly Tyr Phe Tyr Val Gly Leu Asp Tyr Ser
35 40 45

Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile Arg Glu Ser Asn Gly
50 55 60

Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp Gly Lys Ser Val Lys
65 70 75 80

Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile Gly
85 90 95

Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly Ser Val Gly Tyr Gly
100 105 110

Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Arg Phe Lys
115 120 125

Thr Lys Gly Ile Arg Asp Ser Gly Ser Lys Glu Asp Glu Ala Asp Thr
130 135 140

Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp Val Val Thr Gly Gln
145 150 155 160

Thr Asp Asn Leu Ala Ala Ala Leu Ala Lys Thr Ser Gly Lys Asp Leu
165 170 175

Val Gln Phe Ala Asn Ala Val Glu Ile Ser His Ser Glu Ile Gly Lys
180 185 190

Lys Val Cys Val Thr Lys Asn Tyr Asp Ser Gly Ser Asn Phe Ala Lys
195 200 205

Tyr Gly Thr Glu Ser Asn Gly Gln Ser Thr Thr Ser His Arg Val Ala
210 215 220

Leu Cys Gly Gly Lys Gly Val Ala Ser Thr Gly Phe Gly Thr Ala Glu
225 230 235 240

Val Leu Arg Asp Phe Val Arg Glu Thr Leu Leu Ser Asn Gly Ser Lys
245 250 255

Asn Trp Pro Thr Ser Thr Gly Thr Gly Ser Ser Ser Asn Asp Asn Ala
260 265 270

Thr Ala Val Ala Gly Asp Leu Thr Lys Leu Thr Pro Glu Glu Lys Thr
275 280 285

Ile Val Ala Gly Leu Leu Ala Lys Thr Ile Glu Gly Gly Glu Val Val
290 295 300

Glu Ile Arg Ala Val Ser Ser Thr Ser Val Met Val Asn Ala Cys Tyr
305 310 315 320

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Asp Leu Leu Ser Glu Gly Leu Gly Val Val Pro Tyr Ala Cys Val Gly
 325 330 335
 Leu Gly Gly Asn Phe Val Gly Val Val Asp Gly His Ile Thr Pro Lys
 340 345 350
 Leu Ala Tyr Arg Leu Lys Ala Gly Leu Ser Tyr Gln Leu Ser Pro Glu
 355 360 365
 Ile Ser Ala Phe Ala Gly Gly Phe Cys His Arg Val Val Gly Asp Gly
 370 375 380
 Val Tyr Asp Asp Leu Pro Ala Gln Arg Leu Val Asp Asp Thr Ser Pro
 385 390 395 400
 Ala Gly Arg Thr Lys Asp Thr Ala Ile Ala Asn Phe Ser Met Ala Tyr
 405 410 415
 Val Gly Gly Glu Phe Gly Val Arg Phe Ala Phe
 420 425

<210> SEQ ID NO 184
 <211> LENGTH: 429
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 184

Met Arg Lys Gly Lys Ile Ile Leu Gly Ser Val Met Met Ser Met Ala
 1 5 10 15
 Ile Val Met Ala Gly Asn Asp Val Arg Ala His Asp Asp Val Ser Ala
 20 25 30
 Leu Glu Thr Gly Gly Ala Gly Tyr Phe Tyr Val Gly Leu Asp Tyr Ser
 35 40 45
 Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile Arg Glu Ser Asn Gly
 50 55 60
 Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp Gly Lys Ser Val Lys
 65 70 75 80
 Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile Gly
 85 90 95
 Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly Ser Val Gly Tyr Gly
 100 105 110
 Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Arg Phe Lys
 115 120 125
 Thr Lys Gly Val Arg Asp Ser Gly Ser Lys Glu Asp Glu Ala Asp Thr
 130 135 140
 Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp Val Val Thr Gly Gln
 145 150 155 160
 Thr Asp Lys Leu Thr Ala Ala Leu Ala Lys Thr Ser Gly Lys Asp Ile
 165 170 175
 Val Gln Phe Ala Asn Ala Val Lys Ile Ser His Pro Lys Ile Asp Glu
 180 185 190
 Gln Val Cys Ser Lys Asn His Thr Val Leu Asn Pro Ser Gln Gly Thr
 195 200 205
 Thr Tyr Asp Ser Asp Pro Lys Gln Glu Gln Asn Lys Ile Ala Gln Cys
 210 215 220
 Ser Gly Phe Gly Gly Ala Ala Gly Glu Lys Gln Ala Leu Leu Ser Thr
 225 230 235 240
 Phe Ala Ser Ala Val Lys Leu Gly Glu Gly Lys Asn Trp Pro Thr Gly
 245 250 255

-continued

Gln Ala Gly Lys Ser Gly Ser Gly Pro Val Val Gly Ala Pro Asn Ser
260 265 270

Asn Ala Asn Ala Val Ala Lys Asp Leu Val Ala Leu Asn Arg Glu Glu
275 280 285

Lys Thr Ile Val Ala Gly Leu Leu Ala Lys Thr Ile Glu Gly Gly Glu
290 295 300

Val Val Glu Ile Arg Ala Val Ser Ser Thr Ser Val Met Val Asn Ala
305 310 315 320

Cys Tyr Asp Leu Leu Ser Glu Gly Leu Gly Val Val Pro Tyr Ala Cys
325 330 335

Val Gly Leu Gly Gly Asn Phe Val Gly Val Val Asp Gly His Ile Thr
340 345 350

Pro Lys Leu Ala Tyr Arg Leu Lys Ala Gly Leu Ser Tyr Gln Leu Ser
355 360 365

Pro Glu Ile Ser Ala Phe Ala Gly Gly Phe Tyr His Arg Val Val Gly
370 375 380

Asp Gly Val Tyr Asp Asp Leu Pro Ala Gln Arg Leu Val Asp Asp Thr
385 390 395 400

Ser Pro Ala Gly Arg Thr Lys Asp Thr Ala Ile Ala Asn Phe Ser Met
405 410 415

Ala Tyr Val Gly Gly Glu Phe Gly Val Arg Phe Ala Phe
420 425

<210> SEQ ID NO 185
<211> LENGTH: 435
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 185

Met Arg Lys Gly Lys Ile Ile Leu Gly Ser Val Met Met Ser Met Ala
1 5 10 15

Ile Val Met Ala Gly Asn Asp Val Arg Ala His Asp Asp Val Ser Ala
20 25 30

Leu Asp Thr Gly Gly Ala Gly Tyr Phe Tyr Val Gly Leu Asp Tyr Ser
35 40 45

Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile Arg Glu Ser Asn Gly
50 55 60

Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp Gly Lys Ser Val Lys
65 70 75 80

Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile Gly
85 90 95

Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly Ser Val Gly Tyr Gly
100 105 110

Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Arg Phe Lys
115 120 125

Thr Lys Gly Ile Arg Asp Ser Gly Ser Lys Glu Asp Asp Ala Asp Thr
130 135 140

Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp Val Val Thr Gly Gln
145 150 155 160

Thr Asp Asn Leu Ala Ala Ala Leu Ala Lys Thr Ser Gly Lys Asp Ile
165 170 175

Val Gln Phe Ala Lys Thr Leu Asn Ile Ser His Ser Asn Ile Asp Gly
180 185 190

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Lys Val Cys Thr Gly Ser His Ala Asp Leu Ala Pro Gly Thr Asn Ala
 195 200 205
 Gly Lys Lys Phe Val Val Asn Pro Glu Ala Ser Gly Ser Thr Asp Gly
 210 215 220
 Asp Thr Ser Gln Cys Ser Gly Leu Gly His Ser Ser Gly Val Thr Gln
 225 230 235 240
 Asn Pro Lys Leu Phe Ser Thr Phe Val Asp Thr Val Lys Ile Ala Glu
 245 250 255
 Asp Lys Asn Trp Pro Thr Gly Arg Ala Lys Ser Asn Thr Ser Leu Lys
 260 265 270
 Thr Gly Asp Thr Asn Ser Asn Ala Lys Ala Val Ala Thr Asp Leu Thr
 275 280 285
 Lys Leu Thr Ala Glu Glu Lys Thr Ile Val Ala Gly Leu Leu Ala Lys
 290 295 300
 Thr Ile Gly Gly Gly Glu Val Ile Glu Ile Arg Ala Val Ser Ser Thr
 305 310 315 320
 Ser Val Met Val Asn Ala Cys Tyr Asp Leu Leu Ser Glu Gly Leu Gly
 325 330 335
 Val Val Pro Tyr Ala Cys Val Gly Leu Gly Gly Asn Phe Val Gly Val
 340 345 350
 Val Asp Gly His Ile Thr Pro Lys Leu Ala Tyr Arg Leu Lys Ala Gly
 355 360 365
 Leu Ser Tyr Gln Leu Ser Pro Glu Ile Ser Ala Phe Ala Gly Gly Phe
 370 375 380
 Tyr His Arg Val Val Gly Asp Gly Val Tyr Asp Asp Leu Pro Ala Gln
 385 390 395 400
 Arg Leu Val Asp Asp Thr Ser Pro Ala Gly Arg Thr Lys Asp Thr Ala
 405 410 415
 Ile Ala Asn Phe Ser Met Ala Tyr Val Gly Gly Glu Phe Gly Val Arg
 420 425 430
 Phe Ala Phe
 435

<210> SEQ ID NO 186
 <211> LENGTH: 423
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 186

Met Lys His Val Val Cys Lys Asn Cys Val Gly Tyr Val Lys Cys Phe
 1 5 10 15
 Thr Val Arg Cys Ala Tyr Lys Arg Val Leu Tyr Met Val Ser Ala Ile
 20 25 30
 Leu Leu Met Leu Ile Met Gly Glu Asp Ala Lys Ala Val Gly Asp Arg
 35 40 45
 Ala Val Gln Pro Lys Lys Phe Tyr Val Ala Leu Asp Tyr Thr Pro Ala
 50 55 60
 Phe Ser Lys Val Arg Asp Phe Tyr Ile Ser Gly Asp Glu Asn Ser Ala
 65 70 75 80
 Leu Val Met Pro Tyr Pro Lys Ile Lys Glu Glu Asp Val Arg Ala Gln
 85 90 95
 Gly Trp Gly Val Asp Trp Asn Ala Pro Asn Pro Asn Ile Glu Phe Glu
 100 105 110

-continued

Ser Asn Ala Leu Met Ser Trp Glu Gly Ser Leu Gly Tyr Lys Ile Lys
 115 120 125
 Gly Gly Arg Ile Glu Ile Glu Val Gly Tyr Glu Lys Phe Arg Ala Arg
 130 135 140
 Val Ser His Asp Ser Gly Gly Glu Ile His Asp Ala Ala Val Tyr Val
 145 150 155 160
 Phe Met Pro Pro Arg Ala Leu Pro Tyr Phe Val Leu Arg Gly Ser Ser
 165 170 175
 Glu Arg Leu Lys Ser Glu Leu Ser Ser Val Thr Glu Glu Glu Ile Leu
 180 185 190
 Thr Phe Ala Lys Gly Leu Ala Asp Gln Arg Pro Asp Ile Asn Arg Lys
 195 200 205
 Ile Cys Tyr Lys Ala Arg Val Gly Gly Thr Asn Ser His Asn Pro His
 210 215 220
 Val Arg Ala Ala Cys Gln Asp Ser Thr Leu Gly Lys Tyr Val Gly Gly
 225 230 235 240
 Leu Tyr Ala Phe Leu Lys Gly Ala Ile Glu Glu His Ser Ile Trp Ile
 245 250 255
 Ser Glu Gly Ser Gly Gly Arg Val Ala Asn Val Ser Asp Met Val Ser
 260 265 270
 His Ile Arg Ala Leu Thr Pro Glu Glu Lys Glu Ala Leu Ser Gly Ile
 275 280 285
 Leu Ala Ile Ala Thr Gly Tyr Gly Arg Thr Val Glu Val Ser Ser Ile
 290 295 300
 Thr Thr Thr Ser Val Met Val Asn Ala Cys Tyr Asp Arg Asn Ile Lys
 305 310 315 320
 Lys Met Gln Gly Ile Glu Ala Tyr Ala Cys Met Gly Leu Gly Ser Asn
 325 330 335
 Leu Val Glu Val Val Asp Lys His Ile Thr Tyr Lys Phe Ala Tyr Arg
 340 345 350
 Leu Lys Ala Gly Leu Ser Tyr Gln Ile Leu Ser Gly Val Ser Ala Phe
 355 360 365
 Val Gly Gly Phe Tyr His His Val Ile Gly Asn Gly Val Tyr Asp Glu
 370 375 380
 Leu Pro Leu Lys Arg Ile Gly Lys Asp Phe Arg Lys Ala Asp Arg Asn
 385 390 395 400
 Gln Tyr Glu Ala Ile Ala Asn Phe Asp Met Ser Tyr Met Gly Thr Glu
 405 410 415
 Phe Gly Val Arg Phe Ala Phe
 420

<210> SEQ ID NO 187

<211> LENGTH: 416

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 187

Met Val Cys Cys Val Ser Arg Val Val Leu Tyr Ile Ala Ser Val Ile
 1 5 10 15
 Leu Leu Met Leu Ile Met Gly Glu Asp Ala Ser Ala Ala Ile Tyr Lys
 20 25 30
 Asp Asp Leu Pro Pro Asn Ser Lys Lys Phe Tyr Val Ala Leu Asp Tyr
 35 40 45

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Ala Pro Ala Leu Ser Arg Val Ser Thr Phe Asp Ile Val Gly Asp Gly
 50          55          60

Lys Thr His Ile Ala Leu Pro Tyr Leu Lys Asn Asp Gln Glu Asp Arg
65          70          75          80

Phe Asn Ala Glu Ala Ile Asp Trp Asp Ala Pro Asn Leu Ser Val Gln
      85          90          95

Phe Lys Asn Ser Val Leu Met Ser Trp Val Gly Ser Ile Gly Tyr Lys
      100          105          110

Met Met Gly Gly Arg Leu Glu Leu Glu Val Gly His Glu Lys Phe Gly
      115          120          125

Ala Arg Val Ser Ser Gly Glu Asn Arg Glu Glu Asn Ser Asp Val Ala
      130          135          140

Tyr Val Phe Phe Ser Arg Leu Leu Pro Tyr Tyr Leu Val Ser Ala Gln
      145          150          155          160

Tyr Glu Lys Leu Ile Ser Gly Leu Ala Asn Leu Thr Glu Asp Glu Ile
      165          170          175

Leu Ala Phe Ala Asn Gly Val Ala Asp Gln Arg Pro Asp Leu Asp Lys
      180          185          190

Lys Ile Cys Lys Lys Ala Arg Leu Gly Gly Asp Asp Arg Gly Thr Asp
      195          200          205

Ala Gln Ala Ala Cys Arg Asp Ser Ile Lys Gly Ala Asp Val Gly Gly
      210          215          220

Phe Gly Ala Phe Met Arg Lys Ala Ile Gly Thr Tyr Leu Met Trp Arg
      225          230          235          240

Tyr Asn Gly Gly Ser Asp Arg Tyr Gly Leu Glu Arg Gly Gly Arg Ser
      245          250          255

Val Asn Ser Lys Asp Ile Val Ser Asp Ile Lys Glu Leu Pro Lys Glu
      260          265          270

Glu Arg Lys Ile Leu Ala Gly Ile Leu Ala Ala Ala Thr Gly Tyr Gly
      275          280          285

Val Val Val Glu Ile Pro Ser Val Ala Ala Thr Ser Val Met Val Asn
      290          295          300

Ala Cys Tyr Asp His Asn Val Ser Leu Thr Arg Lys Arg Ala Ser Ala
      305          310          315          320

Tyr Ser Cys Val Gly Leu Gly Ser Thr Phe Val Glu Ile Val Asp Glu
      325          330          335

His Arg Ala Ala Lys Leu Ala Tyr Arg Leu Lys Ala Gly Leu Ser Tyr
      340          345          350

Asn Phe Ala Ser Gly Val Thr Ala Phe Val Gly Gly Phe Tyr His His
      355          360          365

Ile Ile Gly Asp Ser Trp Tyr Asp Arg Val Pro Met Arg Thr Val Phe
      370          375          380

Leu Asp Glu Lys Thr Gly Glu Arg Pro Val Lys Thr Gly Lys Val Asp
      385          390          395          400

Leu Ser Leu Asp Tyr Ile Gly Ala Glu Cys Gly Ile Arg Leu Ile Leu
      405          410          415

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<210> SEQ ID NO 188

<211> LENGTH: 254

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

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<222> LOCATION: (144)..(144)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (146)..(146)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (164)..(164)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (166)..(166)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (195)..(195)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (215)..(215)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (222)..(222)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (242)..(242)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 188

gaagaatacg aaagcggcgg agatcggttaa atttgctgag gctgttgga catcgcaaaa    60
ggatattgat aagaaggttt gtaagaagac tggaatgcc gcggacagtt ggaagtgtac    120
gcagactggc agcgacggcg gcancnccaa agagttcagt aaaatattta cgaaggcaga    180
cgtaaatact gacancaaag gcaaagcatg gcctaacggg ancaacgacg ccgcgaaagc    240
ggaagaccta agta                                                    254

<210> SEQ ID NO 189
<211> LENGTH: 257
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 189

gaagaatacg aaagcggcgg agatcggttaa gtttgctgag gctgttgga catcgcaaaa    60
ggatattgat ggaaggtttt gtaagaagac tggaatgag gcggacagtt ggaagtgtac    120
gcagactggc aacggcagcg gcaacgccac agagtttagt aaaatattta cgaagaaaaa    180
cgtagatgct gagggcaaag gcaaagcatg gcctaacggg cacaccgaca gcgccgcgaa    240
agcggaagac ctaagta                                                    257

<210> SEQ ID NO 190
<211> LENGTH: 242
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 190

gaagaatacg aaagcggcgg agatcggttaa gtttgctgag gctgtcgga catcgcaaaa    60
ggatattgat aagaaggtttt gtaagaagac tgaaaataca gaagacagtt ggaagtgtac    120
gcagactggc aacgacggca gcgacaagga gttcagtaaa atatttacga agaaaaacgt    180

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agatactagc ggcaaagcat ggcctaacgg aagcgacgcc gcgaaagcgg aagacctaag 240
ta 242

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<210> SEQ ID NO 191
<211> LENGTH: 242
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 191

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gaagaatacg aaagcggcgg agatcgtaa gtttgctgag gctgttgga catcgcaaa 60
ggatattgat aagaaggttt gtaagaagac tgaaaataca gaagacagtt ggaagtgtac 120
gcagactggc aacgacggcg gcgacaagga gttcagtaaa atatttacga agaaaaacgt 180
agatactagc ggcaaagcat ggcctaacgg aagcgacgcc gcgaaagcgg aagacctaag 240
ta 242

```

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<210> SEQ ID NO 192
<211> LENGTH: 260
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 192

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gaagaatacg aaagcggcgg agatcgtaa atttgctgag gctgttgga catcgcaaa 60
ggatattgat ggaaggttt gtaagaagg cggcagcggc aatgcccgcg gcagctggaa 120
gtgtacgcag actggcagca acggcgtcag caccgcagag ttcagtaaaa tatttacgaa 180
ggcagacgta aatactgaca acaaaggcaa agcatggcct aacgggaaca acgacgctgc 240
gaaagcggaa gacctaagta 260

```

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<210> SEQ ID NO 193
<211> LENGTH: 260
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<400> SEQUENCE: 193

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gaagaatacg aaagcggcgg agatcgtaa atttgctgag gctgttgga catcgcaaa 60
ggatattgat ggaaggttt gtaagaagg cggcagcggc aatgcccgcg gcagctggaa 120
gtgtacgcag actggcagca acggcgtcag caccgcagag ttcagtaaaa tatttacgaa 180
ggcagacgta aatactgaca acaaaggcaa agcacggcct aacgggaaca acgacgctgc 240
gaaagcggaa gacctaagta 260

```

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<210> SEQ ID NO 194
<211> LENGTH: 278
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

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<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (116)..(116)
<223> OTHER INFORMATION: any amino acid

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<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (202)..(202)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (213)..(213)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (214)..(214)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (218)..(218)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (244)..(244)
<223> OTHER INFORMATION: any amino acid

<400> SEQUENCE: 194

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
1      5      10      15

Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Xaa Asp Val Asp
20      25      30

Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
35      40      45

Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
50      55      60

Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
65      70      75      80

Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
85      90      95

Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr
100     105     110

Ser Ile Gly Xaa Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe
115     120     125

Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp
130     135     140

Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp
145     150     155     160

Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu
165     170     175

Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp
180     185     190

Lys Lys Val Cys Lys Lys Thr Gly Asn Xaa Ala Gly Ser Trp Lys Cys
195     200     205

Thr Gln Thr Gly Xaa Xaa Gly Val Ser Xaa Lys Glu Phe Ser Lys Ile
210     215     220

Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala Trp Pro
225     230     235     240

Asn Gly Asn Xaa Asp Ala Ala Lys Ala Glu Asp Leu Ser Ala Leu Asn
245     250     255

Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly Leu Leu Thr
260     265     270

Arg Thr Ile Ser Gly Gly
275

<210> SEQ ID NO 195

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<211> LENGTH: 254
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 195

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
1      5      10      15
Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ala Asp Val Asp
      20      25      30
Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
      35      40      45
Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
      50      55      60
Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
      65      70      75      80
Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
      85      90      95
Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr
      100     105     110
Ser Ile Gly Ile Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe
      115     120     125
Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp
      130     135     140
Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp
      145     150     155     160
Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu
      165     170     175
Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp
      180     185     190
Gly Lys Val Cys Lys Lys Thr Gly Asn Glu Ala Asp Ser Trp Lys Cys
      195     200     205
Thr Gln Thr Gly Asn Gly Ser Gly Asn Ala Thr Glu Phe Ser Lys Ile
      210     215     220
Phe Thr Lys Lys Asn Val Asp Ala Glu Gly Lys Gly Lys Ala Trp Pro
      225     230     235     240
Asn Gly His Thr Asp Ser Ala Ala Lys Ala Glu Asp Leu Ser
      245     250

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<210> SEQ ID NO 196
<211> LENGTH: 298
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 196

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
1      5      10      15
Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp
      20      25      30
Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
      35      40      45
Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
      50      55      60
Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val

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65	70	75	80
Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile	85	90	95
Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr	100	105	110
Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe	115	120	125
Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp	130	135	140
Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp	145	150	155
Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu	165	170	175
Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp	180	185	190
Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala Ala Gly Ser Trp	195	200	205
Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr Ala Glu Phe Ser	210	215	220
Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala	225	230	235
Trp Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu Asp Leu Ser Ile	245	250	255
Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly	260	265	270
Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu Ile Arg Ala	275	280	285
Val Ser Thr Thr Ser Val Met Leu Asn Gly	290	295	

<210> SEQ ID NO 197

<211> LENGTH: 292

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 197

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val	1	5	10	15
Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp	20	25	30	
Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr	35	40	45	
Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr	50	55	60	
Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val	65	70	75	80
Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile	85	90	95	
Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr	100	105	110	
Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe	115	120	125	
Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp				

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130	135	140
Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp		
145	150	155 160
Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu		
	165	170 175
Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp		
	180	185 190
Lys Lys Val Cys Lys Lys Thr Glu Asn Thr Glu Asp Ser Trp Lys Cys		
	195	200 205
Thr Gln Thr Gly Asn Asp Gly Gly Asp Lys Glu Phe Ser Lys Ile Phe		
	210	215 220
Thr Lys Lys Asn Val Asp Thr Ser Gly Lys Ala Trp Pro Asn Gly Ser		
	225	230 235 240
Asp Ala Ala Lys Ala Glu Asp Leu Ser Thr Ala Leu Asn Arg Glu Leu		
	245	250 255
Thr Ser Ala Glu Lys Asn Lys Val Ala Gly Leu Leu Thr Arg Thr Ile		
	260	265 270
Ser Gly Gly Glu Val Val Glu Ile Arg Ala Val Ser Thr Thr Ser Val		
	275	280 285
Met Leu Asn Gly		
290		

<210> SEQ ID NO 198

<211> LENGTH: 298

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 198

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val		
1	5	10 15
Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp		
	20	25 30
Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr		
	35	40 45
Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr		
	50	55 60
Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val		
	65	70 75 80
Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile		
	85	90 95
Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr		
	100	105 110
Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe		
	115	120 125
Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp		
	130	135 140
Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp		
	145	150 155 160
Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu		
	165	170 175
Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp		
	180	185 190
Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala Ala Gly Ser Trp		

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195	200	205
Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr Ala Glu Phe Ser		
210	215	220
Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala		
225	230	235 240
Trp Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu Asp Leu Ser Ile		
	245	250 255
Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly		
	260	265 270
Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu Ile Arg Ala		
	275	280 285
Val Ser Thr Thr Ser Val Met Leu Asn Gly		
290	295	
<210> SEQ ID NO 199		
<211> LENGTH: 298		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic construct		
<400> SEQUENCE: 199		
Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val		
1	5	10 15
Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ser Asp Val Asp		
	20	25 30
Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr		
	35	40 45
Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr		
	50	55 60
Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val		
	65	70 75 80
Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile		
	85	90 95
Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr		
	100	105 110
Ser Ile Gly Val Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe		
	115	120 125
Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp		
	130	135 140
Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp		
	145	150 155 160
Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu		
	165	170 175
Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp		
	180	185 190
Gly Lys Val Cys Lys Lys Gly Gly Ser Gly Asn Ala Ala Gly Ser Trp		
	195	200 205
Lys Cys Thr Gln Thr Gly Ser Asn Gly Val Ser Thr Ala Glu Phe Ser		
	210	215 220
Lys Ile Phe Thr Lys Ala Asp Val Asn Thr Asp Asn Lys Gly Lys Ala		
	225	230 235 240
Arg Pro Asn Gly Asn Asn Asp Ala Ala Lys Ala Glu Asp Leu Ser Ile		
	245	250 255
Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly		

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260	265	270
Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu Ile Arg Ala		
275	280	285
Val Ser Thr Thr Ser Val Met Leu Asn Gly		
290	295	

<210> SEQ ID NO 200
 <211> LENGTH: 396
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (27)..(27)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (77)..(77)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (178)..(178)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (191)..(191)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (203)..(203)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (217)..(217)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (230)..(230)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (233)..(233)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (243)..(243)
 <223> OTHER INFORMATION: any amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (268)..(268)
 <223> OTHER INFORMATION: any amino acid
 <400> SEQUENCE: 200

Met Lys Leu Val Met Met Ser Met Ala Ile Val Met Ala Gly Asn Asp
1 5 10 15
Val Arg Ala His Asp Asp Val Ser Ala Leu Xaa Thr Gly Gly Ala Gly
20 25 30
Tyr Phe Tyr Val Gly Leu Asp Tyr Ser Pro Ala Phe Ser Lys Ile Arg
35 40 45
Asp Phe Ser Ile Arg Glu Ser Asn Gly Glu Thr Lys Ala Val Tyr Pro
50 55 60
Tyr Leu Lys Asp Gly Lys Ser Val Lys Leu Glu Ser Xaa Lys Phe Asp
65 70 75 80
Trp Asn Thr Pro Asp Pro Arg Ile Gly Phe Lys Asp Asn Met Leu Val
85 90 95
Ala Met Glu Gly Ser Val Gly Tyr Gly Ile Gly Gly Ala Arg Val Glu
100 105 110

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Leu Glu Ile Gly Tyr Glu Arg Phe Lys Thr Lys Gly Ile Arg Asp Ser
   115                               120                               125

Gly Ser Lys Glu Asp Glu Ala Asp Thr Val Tyr Leu Leu Ala Lys Glu
   130                               135                               140

Leu Ala Tyr Asp Val Val Thr Gly Gln Thr Asp Lys Leu Leu Ala Ala
   145                               150                               155                               160

Leu Ala Lys Thr Ser Gly Lys Asp Ile Val Gln Phe Ala Glu Ala Val
   165                               170                               175

Gly Xaa Ser Ala Lys Asp Ile Asp Gly Lys Val Cys Lys Lys Xaa Thr
   180                               185                               190

Gly Asn Ala Ala Asp Ser Trp Gln Cys Ser Xaa Gly Ser Gly Gly Ser
   195                               200                               205

Ser Gly Lys Glu Phe Ser Lys Phe Xaa Thr Lys Val Lys Val Asp Glu
   210                               215                               220

Gly Lys Asn Trp Pro Xaa Gly Arg Xaa Ser Ala Ala Lys Asn Asn Ala
   225                               230                               235                               240

Glu Ala Xaa Ala Thr Asp Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys
   245                               250                               255

Thr Ile Val Ala Gly Leu Leu Ala Lys Thr Ile Xaa Gly Gly Glu Val
   260                               265                               270

Val Glu Ile Arg Ala Val Ser Ser Thr Ser Val Met Val Asn Ala Cys
   275                               280                               285

Tyr Asp Leu Leu Ser Glu Gly Leu Gly Val Val Pro Tyr Ala Cys Val
   290                               295                               300

Gly Leu Gly Gly Asn Phe Val Gly Val Val Asp Gly His Ile Thr Pro
   305                               310                               315                               320

Lys Leu Ala Tyr Arg Leu Lys Ala Gly Leu Ser Tyr Gln Leu Ser Pro
   325                               330                               335

Glu Ile Ser Ala Phe Ala Gly Gly Phe Tyr His Arg Val Val Gly Asp
   340                               345                               350

Gly Val Tyr Asp Asp Leu Pro Ala Gln Arg Leu Val Asp Asp Thr Ser
   355                               360                               365

Pro Ala Gly Arg Thr Lys Asp Thr Ala Ile Ala Asn Phe Ser Met Ala
   370                               375                               380

Tyr Val Gly Gly Glu Phe Gly Val Arg Phe Ala Phe
   385                               390                               395

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<210> SEQ ID NO 201
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9) .. (9)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (235) .. (235)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 201

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Tyr Phe Tyr Val Gly Leu Asp Tyr Xaa Pro Ala Phe Ser Lys Ile Asn
 1             5             10             15

Gly Phe Glu Ile Arg Glu Ser Thr Gly Glu Thr Ala Ala Val Tyr Pro
 20             25             30

Tyr Met Lys Asp Gly Thr Arg Val Glu Trp Lys Ala Glu Lys Phe Asp

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35	40	45
Trp Asn Thr Pro Asp Pro Arg Ile Lys Phe Lys Asn Asn Pro Ile Val 50 55 60		
Ala Leu Glu Gly Ser Val Gly Tyr Ser Ile Gly Val Ala Arg Val Glu 65 70 75 80		
Leu Glu Ile Gly Tyr Glu Gln Phe Lys Thr Lys Gly Ile Arg Asp Thr 85 90 95		
Gly Ser Lys Glu Glu Glu Ala Asp Ala Val Tyr Leu Leu Ala Lys Lys 100 105 110		
Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe Leu Glu Glu 115 120 125		
Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val 130 135 140		
Gly Thr Ser Ala Lys Asp Ile Asp Lys Lys Val Cys Lys Lys His Thr 145 150 155 160		
Asn Asn Ala Ala Asn Ser Trp Lys Cys Glu Gln Pro Gly Ser Lys Gly 165 170 175		
Lys Ala Trp Pro Asn Gly His Thr Asp Ser Ala Ala Lys Ala Glu Asp 180 185 190		
Leu Ser Thr Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys 195 200 205		
Val Ala Gly Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu 210 215 220		
Ile Arg Ala Val Ser Thr Thr Ser Val Met Xaa Asn Ala Cys Tyr Asp 225 230 235 240		
Leu Leu Ser		

<210> SEQ ID NO 202

<211> LENGTH: 259

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 202

Tyr Phe Tyr Val Gly Leu Asp Tyr Cys Pro Ala Phe Ser Lys Ile Asn 1 5 10 15
Gly Phe Glu Ile Arg Glu Ser Thr Gly Glu Thr Ala Ala Val Tyr Pro 20 25 30
Tyr Met Lys Asp Gly Thr Arg Val Glu Trp Lys Ala Glu Lys Phe Asp 35 40 45
Trp Asn Thr Pro Asp Pro Arg Ile Lys Phe Lys Asn Asn Pro Ile Val 50 55 60
Ala Leu Glu Gly Ser Val Gly Tyr Ser Ile Gly Val Ala Arg Val Glu 65 70 75 80
Leu Glu Ile Gly Tyr Glu Gln Phe Lys Thr Lys Gly Ile Arg Asp Thr 85 90 95
Gly Ser Lys Glu Glu Glu Ala Asp Ala Val Tyr Leu Leu Ala Lys Lys 100 105 110
Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe Leu Glu Glu 115 120 125
Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val 130 135 140
Gly Thr Ser Ala Lys Asp Ile Asp Gly Lys Val Cys Lys Lys His Asn 145 150 155 160

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Gly Asn Ala Ala Gly Ser Trp Gln Cys Thr Gln Thr Gly Ser Glu Thr
 165 170 175

Ser Gly Lys Thr Leu Ser Glu Ile Phe Thr Lys Ala Gly Val Asp Ala
 180 185 190

Asn Gly Lys Ala Trp Pro Asn Gly Ser Asp Ala Ala Lys Ala Glu Asp
 195 200 205

Leu Ser Thr Ala Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys
 210 215 220

Val Ala Gly Leu Leu Thr Arg Thr Ile Ser Gly Gly Glu Val Val Glu
 225 230 235 240

Ile Arg Ala Val Ser Thr Thr Ser Val Met Ile Asn Ala Cys Tyr Asp
 245 250 255

Leu Leu Ser

<210> SEQ ID NO 203
 <211> LENGTH: 263
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 203

Tyr Phe Tyr Val Gly Leu Asp Tyr Ser Pro Ala Phe Ser Lys Ile Asn
 1 5 10 15

Gly Phe Glu Ile Arg Glu Ser Thr Gly Glu Thr Ala Ala Val Tyr Pro
 20 25 30

Tyr Met Lys Asp Gly Thr Arg Val Glu Trp Lys Ala Glu Lys Phe Asp
 35 40 45

Trp Asn Thr Pro Asp Pro Arg Ile Lys Phe Lys Asn Asn Pro Ile Val
 50 55 60

Ala Leu Glu Gly Ser Val Gly Tyr Ser Ile Gly Val Ala Arg Val Glu
 65 70 75 80

Leu Glu Ile Gly Tyr Glu Gln Phe Lys Thr Lys Gly Ile Arg Asp Thr
 85 90 95

Gly Ser Lys Glu Glu Glu Ala Asp Ala Val Tyr Leu Leu Ala Lys Lys
 100 105 110

Leu Pro His Thr Leu Val Ser Asp Gln Ser Asp Lys Phe Leu Glu Glu
 115 120 125

Leu Lys Asn Thr Lys Ala Ala Glu Ile Val Lys Phe Ala Glu Ala Val
 130 135 140

Gly Thr Ser Ala Lys Asp Ile Asp Gly Lys Val Cys Lys Lys Asn Thr
 145 150 155 160

Asn Asn Ala Ala Asp Ser Trp Lys Cys Glu Gln Thr Gly Ser Gly Ser
 165 170 175

Asp Gly Lys Glu Phe Ser Lys Leu Phe Thr Lys Ala Gly Val Asp Ala
 180 185 190

Asn Glu Lys Gly Lys Ala Trp Pro Asn Gly His Thr Asp Ser Ala Ala
 195 200 205

Lys Ala Glu Asp Leu Ser Thr Ala Leu Asn Arg Glu Leu Thr Ser Ala
 210 215 220

Glu Lys Asn Lys Val Ala Gly Leu Leu Thr Arg Thr Ile Ser Gly Gly
 225 230 235 240

Glu Val Val Glu Ile Arg Ala Val Ser Thr Thr Ser Val Met Leu Asn
 245 250 255

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Ala Cys Tyr Asp Leu Leu Ser
260

<210> SEQ ID NO 204
 <211> LENGTH: 280
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 204

Met Lys Glu Arg Lys Leu Ala Leu Ser Gly Ala Val Ala Met Thr Val
 1 5 10 15
 Leu Val Ser Thr Ala Gly Thr Gly Thr Ala Ala Gly Ala Asp Val Asp
 20 25 30
 Tyr Val Ser Lys Phe Gly Glu Gly Ser Phe Tyr Val Gly Leu Asn Tyr
 35 40 45
 Ser Pro Ala Phe Ser Lys Ile Asn Gly Phe Glu Ile Arg Glu Ser Thr
 50 55 60
 Gly Glu Thr Ala Ala Val Tyr Pro Tyr Met Lys Asp Gly Thr Arg Val
 65 70 75 80
 Glu Trp Lys Ala Glu Lys Phe Asp Trp Asn Thr Pro Asp Pro Arg Ile
 85 90 95
 Lys Phe Lys Asn Asn Pro Ile Val Ala Leu Glu Gly Ser Val Gly Tyr
 100 105 110
 Ser Ile Gly Ile Ala Arg Val Glu Leu Glu Ile Gly Tyr Glu Gln Phe
 115 120 125
 Lys Thr Lys Gly Ile Arg Asp Thr Gly Ser Lys Glu Glu Glu Ala Asp
 130 135 140
 Ala Val Tyr Leu Leu Ala Lys Lys Leu Pro His Thr Leu Val Ser Asp
 145 150 155 160
 Gln Ser Asp Lys Phe Leu Glu Glu Leu Lys Asn Thr Lys Ala Ala Glu
 165 170 175
 Ile Val Lys Phe Ala Glu Ala Val Gly Thr Ser Ala Lys Asp Ile Asp
 180 185 190
 Gly Lys Val Cys Lys Lys Thr Gly Asn Glu Ala Asp Ser Trp Lys Cys
 195 200 205
 Thr Gln Thr Gly Asn Gly Ser Gly Asn Ala Thr Glu Phe Ser Lys Ile
 210 215 220
 Phe Thr Lys Lys Asn Val Asp Ala Glu Gly Lys Gly Lys Ala Trp Pro
 225 230 235 240
 Asn Gly His Thr Asp Ser Ala Ala Lys Ala Glu Asp Leu Ser Thr Ala
 245 250 255
 Leu Asn Arg Glu Leu Thr Ser Ala Glu Lys Asn Lys Val Ala Gly Leu
 260 265 270
 Leu Thr Arg Thr Ile Ser Gly Gly
 275 280

<210> SEQ ID NO 205
 <211> LENGTH: 431
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 205

Met Arg Lys Gly Lys Ile Ile Leu Gly Ser Val Met Met Ser Met Ala
 1 5 10 15

Ile	Val	Met	Ala	Gly	Asn	Asp	Val	Arg	Ala	His	Asp	Asp	Val	Ser	Ala
			20					25					30		
Leu	Glu	Thr	Gly	Gly	Ala	Gly	Tyr	Phe	Tyr	Val	Gly	Leu	Asp	Tyr	Ser
		35					40					45			
Pro	Ala	Phe	Ser	Lys	Ile	Arg	Asp	Phe	Ser	Ile	Arg	Glu	Ser	Asn	Gly
	50					55					60				
Glu	Thr	Lys	Ala	Val	Tyr	Pro	Tyr	Leu	Lys	Asp	Gly	Lys	Ser	Val	Lys
65					70					75					80
Leu	Glu	Ser	His	Lys	Phe	Asp	Trp	Asn	Thr	Pro	Asp	Pro	Arg	Ile	Gly
				85					90					95	
Phe	Lys	Asp	Asn	Met	Leu	Val	Ala	Met	Glu	Gly	Ser	Val	Gly	Tyr	Gly
			100					105					110		
Ile	Gly	Gly	Ala	Arg	Val	Glu	Leu	Glu	Ile	Gly	Tyr	Glu	Arg	Phe	Lys
		115					120					125			
Thr	Lys	Gly	Ile	Arg	Asp	Ser	Gly	Ser	Lys	Glu	Asp	Glu	Ala	Asp	Thr
	130					135					140				
Val	Tyr	Leu	Leu	Ala	Lys	Glu	Leu	Ala	Tyr	Asp	Val	Val	Thr	Gly	Gln
145					150					155					160
Thr	Asp	Asn	Leu	Ala	Ala	Ala	Leu	Ala	Lys	Thr	Ser	Gly	Lys	Asp	Ile
				165					170					175	
Val	Gln	Phe	Ala	Lys	Ala	Val	Glu	Ile	Ser	Asn	Ser	Gly	Ile	Gly	Lys
			180					185					190		
Lys	Val	Cys	Glu	Thr	Lys	Arg	Lys	Asp	Gly	Asp	Thr	Thr	Asn	Arg	Phe
	195						200					205			
Ala	Lys	Tyr	Ile	Val	Gly	Ala	Gly	Asp	Ser	Ser	Asn	Ala	Gly	Thr	Ser
	210					215					220				
Leu	Cys	Gly	Gly	Lys	Asn	Gln	Lys	Ser	Ser	Asp	Thr	Asp	Thr	Gly	Val
225					230					235					240
Glu	Lys	Ala	Gln	Ala	Leu	His	Asp	Phe	Val	Ser	Asn	Thr	Leu	Ser	Asp
				245					250					255	
Gly	Thr	Lys	Asn	Trp	Pro	Thr	Ser	Ser	Glu	Thr	Ser	Lys	Ser	Asn	Asn
			260					265					270		
Asp	Asn	Ala	Lys	Ala	Val	Ala	Gly	Asp	Leu	Thr	Lys	Lys	Leu	Thr	Pro
	275						280					285			
Glu	Glu	Lys	Thr	Ile	Val	Ala	Gly	Leu	Leu	Ala	Lys	Thr	Ile	Glu	Gly
	290					295					300				
Gly	Glu	Val	Val	Glu	Ile	Arg	Ala	Val	Ser	Ser	Thr	Ser	Val	Met	Val
305					310					315					320
Asn	Ala	Cys	Tyr	Asp	Leu	Leu	Ser	Glu	Gly	Leu	Gly	Val	Val	Pro	Tyr
			325						330					335	
Ala	Cys	Val	Gly	Leu	Gly	Gly	Asn	Phe	Val	Gly	Val	Val	Asp	Gly	His
			340					345					350		
Ile	Thr	Pro	Lys	Leu	Ala	Tyr	Arg	Leu	Lys	Ala	Gly	Leu	Ser	Tyr	Gln
		355					360					365			
Leu	Ser	Pro	Glu	Ile											

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<210> SEQ ID NO 206
<211> LENGTH: 433
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 206

Met Met Ser Met Ala Ile Val Met Ala Gly Ser Asp Val Arg Ala His
 1             5             10             15
Asp Asp Val Ser Ala Leu Asp Thr Gly Gly Ala Gly Tyr Phe Tyr Val
 20             25             30
Gly Leu Asp Tyr Ser Pro Ala Phe Ser Lys Ile Arg Asp Phe Ser Ile
 35             40             45
Arg Glu Ser Asn Gly Glu Thr Lys Ala Val Tyr Pro Tyr Leu Lys Asp
 50             55             60
Gly Lys Ser Val Lys Leu Glu Ser His Lys Phe Asp Trp Asn Thr Pro
 65             70             75             80
Asp Pro Arg Ile Gly Phe Lys Asp Asn Met Leu Val Ala Met Glu Gly
 85             90             95
Ser Val Gly Tyr Gly Ile Gly Gly Ala Arg Val Glu Leu Glu Ile Gly
 100            105            110
Tyr Glu Arg Phe Lys Thr Lys Gly Ile Arg Asp Ser Gly Ser Lys Glu
 115            120            125
Asp Glu Ala Asp Thr Val Tyr Leu Leu Ala Lys Glu Leu Ala Tyr Asp
 130            135            140
Val Val Thr Gly Gln Thr Asp Lys Leu Thr Ala Ala Leu Ala Lys Thr
 145            150            155            160
Ser Gly Lys Asp Ile Val Gln Phe Ala Lys Thr Leu Gly Ile Ser His
 165            170            175
Ser Glu Ile Asp Lys Lys Val Cys Ser Gly Ser His Ala Lys Gly Asn
 180            185            190
Ser Glu Thr Thr Lys Asn Asn Thr Val Ala Ser Tyr Thr Glu Lys Pro
 195            200            205
Thr Ala Ala Thr Ala Thr Ala Gln Cys Ser Gly Phe Pro Asp Glu Ala
 210            215            220
Ala Gly Asn Lys Ala Gly Gly Leu Asn Arg Phe Val Ser Glu Thr Lys
 225            230            235            240
Val Glu Glu Gly Lys Asn Trp Pro Thr Gly Lys Ile His Ser Gly Ser
 245            250            255
Ser Thr Asn Asn Val Asp Gly Thr His Asn Gly Asn Ala Lys Ala Val
 260            265            270
Ala Thr Asp Leu Val Asn Leu Asn Arg Asp Glu Lys Thr Ile Val Ala
 275            280            285
Gly Leu Leu Ala Lys Thr Ile Glu Gly Gly Glu Val Val Glu Ile Arg
 290            295            300
Ala Val Ser Ser Thr Ser Val Met Val Asn Ala Cys Tyr Asp Leu Leu
 305            310            315            320
Ser Glu Gly Leu Gly Val Val Pro Tyr Ala Cys Val Gly Leu Gly Gly
 325            330            335
Asn Phe Val Gly Val Val Asp Gly His Ile Thr Pro Lys Leu Ala Tyr
 340            345            350
Arg Leu Lys Ala Gly Leu Ser Tyr Gln Leu Ser Pro Glu Ile Ser Ala
 355            360            365

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Phe Ala Gly Gly Phe Tyr His Arg Val Val Gly Asp Gly Val Tyr Asp
 370                      375                      380

Asp Leu Pro Ala Gln Arg Leu Val Asp Asp Thr Ser Pro Ala Gly Arg
385                      390                      395                      400

Thr Lys Asp Thr Ala Ile Ala Asn Phe Ser Met Ala Tyr Val Gly Ala
                      405                      410                      415

Ser Phe Gln Pro Tyr Tyr Ala Val Leu Leu Val Glu Leu Tyr Glu Tyr
 420                      425                      430

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Arg

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<210> SEQ ID NO 207
<211> LENGTH: 1230
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (34)..(34)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (40)..(40)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (49)..(49)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (55)..(55)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (58)..(58)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(60)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (66)..(66)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (71)..(72)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (87)..(87)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (98)..(98)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (107)..(108)
<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
<222> LOCATION: (110)..(110)
<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: a, c, g or t
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<223> OTHER INFORMATION: a, c, g or t
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<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: a, c, g or t
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<223> OTHER INFORMATION: a, c, g or t
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<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: a, c, g or t
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<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (246)..(246)
<223> OTHER INFORMATION: n is a, c, g, or t
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<221> NAME/KEY: misc_feature
<222> LOCATION: (252)..(252)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (282)..(282)
<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
<222> LOCATION: (315)..(316)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (324)..(324)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (345)..(345)
<223> OTHER INFORMATION: a, c, g or t
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<223> OTHER INFORMATION: a, c, g or t
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<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
<222> LOCATION: (372)..(372)
<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
<222> LOCATION: (390)..(390)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (396)..(396)
<223> OTHER INFORMATION: a, c, g or t
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<221> NAME/KEY: misc_feature
<222> LOCATION: (399)..(399)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (407)..(407)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (411)..(411)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (429)..(429)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (433)..(433)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (462)..(462)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (469)..(469)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (471)..(471)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (474)..(474)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (480)..(480)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (485)..(486)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (492)..(492)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (507)..(507)
<223> OTHER INFORMATION: a, c, g or t
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agagagagta ncgnganac tanggcagta tatccgtaca tgaaagatgg aantagngtg	240
gagttnaagg cncacaagtt cgactggaac acaccagatc cnaggattag gtttaaggac	300
aacatgctcg tagcnntaga aggnagtgtt gggtagacgta ttgngggagc cagggttgaa	360
ctngagatng gntatgaacg gttcaagacn aagggnatna gagatanggg nagtaaggaa	420
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ngcatgncct aacangaaca atgncactan gaacagcgaa aggnctaant aataacgttn	780
antaanaanc tnaccannga ngaaaagacc atagtagctg ggntactagc taggactatt	840
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<211> LENGTH: 1224

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<212> TYPE: DNA
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gagggtctat ttccaggcgc cggagccggg agtttttaca taggactgga ctacagccca    180
gcattcggca gcatcaagga ctttaaagtc caagaggctg gcggcactac tagagggtgtg    240
ttcccgtaga agcgagatgc tgcaggctcg gtggatttca aggtccacaa cttegactgg    300
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gtgagccaga atgtgtgcaa gggtagctgt agcactggca gcagtggcaa caaatgtggt    660
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<210> SEQ ID NO 209
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 <223> OTHER INFORMATION: Synthetic construct

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ttctatgttg gtttgatta cagtcacgag tttagcaaga taagagattt tagtataagg    180
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ctagagtcac acaagtttga ctggaacaca cctgacctc ggattgggtt taaggacaac    300
atgctttagt ctatggaagg cagtgttggg tacgggtattg gtggtgccag ggttgagctt    360
gagattggtt acgagcgctt caagaccaag ggtattagag atagtggtag taaggagat    420
gaagcagata cagtatatct actagctaag gagttagctt atgatgttgt tactgggcag    480
actgataacc ttgccgtgc tcttgccaaa acctcaggta aggacatcgt tcagtttgct    540
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gagaaggctc aggtcttgca tgactttgtt tctaacacat tgagtgatgg tactaagaac	780
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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

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agcagcgtat catgaaggga atgagccaga atcagctggc tagtagattg ggaattactt	180
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agacatcctt agaggagttc aaccacaact acaacgacgg taaggaagtt ctgatgcttg	420
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tcctaaactg gcttacaagg tcaaggctgg tttgagttat gagtgtgcg cggaatctc	3540
aatgttcgct ggtgggttct atcatcgggt gctgggtgaa ggtgagtacg atgatctgcc	3600
agtgcagagg cttgtagacg atgcgactac gaacaagact aaagagttcg ctaaagcgtc	3660
gttcaagatg gcgtacactg gtgctgaaat cgggtgttag tctgcgttct aatgcgcagt	3720

-continued

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gcatggcggg cttaggcccg ccatgattta accctgactg tagaaagcta actagaagga 3780
aagagatgaa gcgagtttgt gttgtgacaa gtttgatgtt agtggcgctg actagtacaa 3840
cgcaaaactaa tgctcggagt actaaagtac aacctacgag ccaagatctg tatgtcgggt 3900
taagttacag tccggcatgg caaagataac tgacttcaac atcggagcga acga 3954

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<210> SEQ ID NO 211
<211> LENGTH: 324
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (239)..(239)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (264)..(264)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (287)..(287)
<223> OTHER INFORMATION: any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (299)..(299)
<223> OTHER INFORMATION: any amino acid

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<400> SEQUENCE: 211

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Met Lys Lys Arg Ile Arg Val Phe Ala Phe Ala Val Phe Met Leu Gly
 1             5             10            15
Leu Pro Ser Val Ser Phe Ala Ser Pro Gln Pro Val Asp Phe Ser Tyr
          20          25          30
His Glu Gly Ala Ser Gly Phe Phe Ala Ser Val Gln Tyr Lys Tyr Gly
          35          40          45
Ala Pro Tyr Phe Gly Ser Leu Thr Leu Glu Ser Gly Gly Lys Thr Leu
          50          55          60
Asn Leu Val Ser Ala Val Gln Glu Lys Lys Pro Pro Glu Ala Pro Ala
          65          70          75          80
Ala Asp Glu Ala Ala Gly Pro Ala Thr Pro Ala Pro Ser Ser Pro Glu
          85          90          95
Gly Phe Gly Ser Ser Thr Asp Asp Phe Gln Gly Arg Tyr Ser Pro Thr
          100         105         110
Tyr Leu Lys Asp Ala Gly Ala Phe Ser Ile Thr Ala Gly Tyr Thr Thr
          115         120         125
Gly Ile Met Arg Phe Glu Ala Glu Ala Met Arg Ser Arg Phe Gln Val
          130         135         140
Asn Gly Ser Lys Trp Asn Pro Val Glu Asn Ala Tyr Ile Phe Ala Ala
          145         150         155         160
Ala Lys Pro Ser Glu Asn Ile Ser Tyr Pro Ala Gln Ile Leu Glu Ala
          165         170         175
Gln Lys Tyr Phe Val Thr Leu Glu Asn Arg Asp Val Ala Ile Thr Ser
          180         185         190
Leu Val Ala Asn Ala Cys Tyr Asp Met Met Pro Ala Thr Ser Ser Ile
          195         200         205
Ala Pro Ser Ala Cys Val Gly Val Gly Val Ser Phe Ala Lys Leu Leu
          210         215         220
Gly Val Leu Glu Gln Arg Leu Thr Tyr Gln Phe Lys Gly Gly Xaa Gln
          225         230         235         240

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[illegible]

```
<210> SEQ ID NO 212
<211> LENGTH: 324
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
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<400> SEQUENCE: 212

Met 1	Lys	Lys	Arg	Ile 5	Arg	Val	Phe	Ala	Phe 10	Ala	Val	Phe	Met	Leu 15	Gly
Leu	Pro	Ser	Val 20	Ser	Phe	Ala	Ser	Pro 25	Gln	Pro	Val	Asp 30	Phe	Ser	Tyr
His	Glu	Gly 35	Ala	Ser	Gly	Phe	Phe 40	Ala	Ser	Val	Gln	Tyr 45	Lys	Tyr	Gly
Ala	Pro 50	Tyr	Phe	Gly	Ser	Leu 55	Thr	Leu	Glu	Ser	Gly 60	Gly	Lys	Ile	Leu
Asn 65	Leu	Val	Ser	Ala	Val 70	Gln	Glu	Lys	Lys	Pro 75	Pro	Glu	Ala	Pro	Ala 80
Ala	Asp	Glu	Ala	Ala 85	Gly	Pro	Ala	Thr	His 90	Ala	Pro	Ser	Ser	Pro 95	Glu
Gly	Phe	Gly	Ser 100	Ser	Thr	Asp	Asp	Phe 105	Gln	Gly	Arg	Tyr 110	Ser	Pro	Thr
Tyr	Leu	Lys 115	Asp	Ala	Gly	Ala	Phe 120	Ser	Ile	Thr	Ala	Gly 125	Tyr	Thr	Thr
Gly	Ile 130	Met	Arg	Phe	Glu	Ala 135	Glu	Ala	Met	Arg	Ser 140	Arg	Phe	Gln	Val
Asn 145	Gly	Ser	Lys	Trp	Asn 150	Pro	Val	Glu	Asn	Ala 155	Tyr	Ile	Phe	Ala	Ala 160
Ala	Lys	Pro	Ser	Glu 165	Asn	Ile	Ser	Tyr	Pro 170	Ala	Gln	Ile	Leu	Glu 175	Thr
Gln	Lys	Tyr	Phe 180	Val	Thr	Leu	Glu	Asn 185	Arg	Asp	Val	Ala	Ile 190	Thr	Ser
Leu	Val	Ala 195	Ser	Ala	Cys	Tyr	Asp 200	Met	Met	Pro	Ala	Thr 205	Ser	Ser	Ile
Ala	Pro 210	Ser	Ala	Cys	Val	Gly 215	Val	Gly	Val	Ser	Phe 220	Ala	Lys	Leu	Leu
Gly 225	Val	Leu	Glu	Gln	Arg 230	Leu	Thr	Tyr	Gln	Phe 235	Lys	Gly	Gly	Leu	Gln 240
Tyr	Phe	Val	Gly 245	Lys	Lys	Thr	Val	Ile	Phe 250	Leu	Ser	Gly	Tyr	Val 255	Ser
Thr	Ile	Gly	Gly 260	Arg	Lys	Ile	Ser	Gln 265	Val	Lys	Val	Lys	His 270	Arg	Leu
Pro	Thr	Pro	Gln	Thr	Ala	Ser	Val	Gly	Ala	Glu	Gly	Ser	Gly	Ser	Gly

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275	280	285
Ala Ala Ala Thr Ser Ser	Ala Pro Pro Ala Leu Ile His Leu Leu Tyr	
290	295	300
Pro Asp Ala Asn Leu Ser	Leu Ala Tyr Tyr Gly Phe Glu Leu Gly Val	
305	310	315 320
Arg Leu Val Phe		

What is claimed is:

1. A method for diagnosing an infection with *Anaplasma platys* in a subject comprising the steps of: (a) providing a test sample from the subject; (b) providing an isolated or purified P44 protein of *Anaplasma platys*; (c) contacting the test sample with the P44 protein; and (d) assaying for the formation of a complex between antibodies in the test sample and the P44 protein, wherein formation of said

complex is indicative of infection with *Anaplasma platys*, wherein the *Anaplasma platys* P44 protein comprises SEQ ID NO: 39, SEQ ID NO: 92 or SEQ ID NO:44.

2. The method of claim 1, wherein the *Anaplasma platys* P44 protein comprises SEQ ID NO: 39 or SEQ ID NO: 44.

3. The method of claim 1, wherein the test sample comprises a serum sample or a plasma sample.

* * * * *